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OM nucleic - nucleic search, using sw model

Run on: January 31, 2006, 08:47:30 ; Search time 5312 Seconds
(without alignments)
11278.802 Million cell updates/sec

Title: US-09-965-703A-3
Perfect score: 1054
Sequence: 1 cctgagtgctgtacccga.....gtccggccgcgtgctctga 1054

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: gb_ba:**
- 2: gb_in:**
- 3: gb_env:**
- 4: gb_om:**
- 5: gb_ov:**
- 6: gb_pat:**
- 7: gb_ph:**
- 8: gb_pr:**
- 9: gb_ro:**
- 10: gb_sts:**
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- 12: gb_un:**
- 13: gb_vi:**
- 14: gb_htg:**
- 15: gb_pl:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1054	100.0	1054	6	AX256355 Sequence
2	1054	100.0	1288	6	AX256353 Sequence
3	1054	100.0	3962	2	CFU29531
4	1054	100.0	6852	2	AF092030 Choriston
5	1029.4	97.7	1290	6	AX407011 Sequence
6	1010.2	95.8	1073	6	AX407021 Sequence
7	1005	95.4	1110	6	AX256354 Sequence
8	1005	95.4	1542	6	AX256401 Sequence
9	960	91.1	960	6	AX256357 Sequence
10	929	88.1	1247	6	AX256414 Sequence
11	735	69.7	735	6	AX256356 Sequence
12	683.6	64.9	6083	2	AY489269 Plodia in
13	652.4	61.9	1017	2	PCO251809
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23	617.2	58.6	1848	6	AX555382	AX555382 Sequence
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ALIGNMENTS

RESULT 1
AX256355
LOCUS AX256355 1054 bp DNA linear PAT 10-OCT-2001
DEFINITION Sequence 3 from Patent WO0170816.
ACCESSION AX256355
VERSION AX256355.1 GI:16075206
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 other sequences; artificial sequences.
AUTHORS Palli,S.R., Kapitskaya,M.Z. and Cress,D.E.
TITLE Bcdysone receptor-based inducible gene expression system
JOURNAL Patent: WO 0170816-A 3 27-SEP-2001;
ROHM AND HAAS COMPANY (US)
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source Location/Qualifiers
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ORIGIN

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RESULT 2
AX256353
LOCUS 1288 bp DNA linear PAT 10-OCT-2001
DEFINITION Sequence 1 from Patent WO0170816.
ACCESSION AX256353
VERSION AX256353.1 GI:16075204
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Palli,S.R., Kapitskaya,M.Z. and Cross,D.E.
TITLE Ecdysone receptor-based inducible gene expression system
JOURNAL Patent: WO 0170816-A 1 27-SEP-2001;
ROHM AND HAAS COMPANY (US)

FEATURES
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Location/Qualifiers
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/organism="synthetic construct"
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ORIGIN
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Best Local Similarity 100.0%; Pred. NO. 1.9e-244;
Matches 1054; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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955 GAGCAGCGCAACTGTTGGAAGAAATCCAGCGGTACTACTGAAATACGCTCCGATCTAT 1014
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RESULT 3
LOCUS CFU29531
DEFINITION Choristoneura fumiferana ecdysteroid receptor Ecr-B mRNA, complete cds.
ACCESSION U29531
VERSION U29531.2
KEYWORDS GI:5731355
SOURCE Choristoneura fumiferana (spruce budworm)
ORGANISM Choristoneura fumiferana
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Tortricidae; Tortricinae; Choristoneura.
REFERENCE 1 (bases 1 to 3960)
AUTHORS Kothapalli, R., Palli, S. R., Ladd, T. R., Sohi, S. S., Cress, D.,
Dhadialla, T. S., Tzertzinis, G. and Retnakaran, A.
TITLE Cloning and developmental expression of the ecdysone receptor gene
from the spruce budworm, Choristoneura fumiferana
JOURNAL Dev. Genet. 17 (4), 319-330 (1995)
PUBMED 8641050
REFERENCE 2 (bases 1 to 3960)
AUTHORS Kothapalli, R., Palli, S. R., Ladd, T. and Retnakaran, A.
TITLE Direct Submission
JOURNAL Submitted (20-JUN-1995) Subba Reddy Palli, Molecular Entomology,
CPS-Sault Ste. Marie, 1219 Queen Street East, Sault Ste. Marie, ONT
P6A S7, Canada
REFERENCE 3 (bases 1 to 3960)
AUTHORS Kothapalli, R., Palli, S. R., Ladd, T. and Retnakaran, A.
TITLE Direct Submission
JOURNAL Submitted (22-SEP-1998) Subba Reddy Palli, Molecular Entomology,
CPS-Sault Ste. Marie, 1219 Queen Street East, Sault Ste. Marie, ONT
P6A S7, Canada
REMARK Sequence update by submitter
REFERENCE 4 (bases 1 to 3962)
AUTHORS Palli, R.
TITLE Direct Submission
JOURNAL Submitted (12-AUG-1999) Rohm and Haas Research Labs, 727 Norristown
Road, PO Box 904, Spring House, PA 19477, USA
REMARK Sequence update by submitter
COMMENT On Aug 12, 1999 this sequence version replaced gi:3641616.
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ORIGIN

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DEFINITION	Choristoneura fumiferana ecdysone receptor isoform A (Ecr) mRNA, complete cds.						
ACCESSION	AF092030						
VERSION	AF092030.2	GI:5713321					
KEYWORDS							
SOURCE	Choristoneura fumiferana (spruce budworm)						
ORGANISM	Choristoneura fumiferana						
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REFERENCE	1 (bases 1 to 6852)						
AUTHORS	Perera, S.C., Ladd, T.R., Dhadialla, T.S., Krell, P.J., Sohi, S.S., Retnakaran, A. and Palli, S.R.						
TITLE	Studies on two ecdysone receptor isoforms of the spruce budworm, Choristoneura fumiferana						
JOURNAL	Mol. Cell. Endocrinol. 152 (1-2), 73-84 (1999)						
PUBMED	10432225						
REFERENCE	2 (bases 1 to 6852)						
AUTHORS	Perera, S.C., Ladd, T.R., Dhadialla, T.S., Krell, P.J., Sohi, S.S., Retnakaran, A. and Palli, S.R.						
TITLE	Direct Submission						
JOURNAL	Submitted (14-SEP-1998) Great Lakes Forestry Centre, Canadian Forest Service, 1219 Queen Street East, Sault Ste. Marie, Ontario P6A 5M7, Canada						
REFERENCE	3 (bases 1 to 6852)						
AUTHORS	Perera, S.C., Ladd, T.R., Dhadialla, T.S., Krell, P.J., Sohi, S.S., Retnakaran, A. and Palli, S.R.						
TITLE	Direct Submission						
JOURNAL	Submitted (09-AUG-1999) Great Lakes Forestry Centre, Canadian Forest Service, 1219 Queen Street East, Sault Ste. Marie, Ontario P6A 5M7, Canada						
REMARK	Sequence update by submitter						
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ORIGIN							
Query Match	100.0%;	Score 1054;	DB 2;	Length 6852;			
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Matches 1054;	Conservative 0;						
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		1212	CAGCAGTTTCTTATGCGCAGGCTCATCTGTTACCAAGCAGCGGTACGAGCAGCTTCTGAT	1271			
		301	GAAGATTTTGAAGAGGATTATCCACAGACGTGGCAGCAGCGGACGATGAAAAACGAAAGAGTCT	360			
		1272	GAAGATTTTGAAGAGGATTATCCACAGACGTGGCAGCAGCGGACGATGAAAAACGAAAGAGTCT	1331			
		361	GACATCTCCCTTCGCGCAGATCACAGAGATGATATCTCTCAAGTCCAGTTCATTCGTGGAG	420			
		1332	GACATCTCCCTTCGCGCAGATCACAGAGATGATATCTCTCAAGTCCAGTTCATTCGTGGAG	1391			
		421	TTTCGGAAGGATTTGCCCAGGTTTCGCAGAGTCTCGCAGGCTGATCAAAATTCAGCTGCTT	480			
		1392	TTTCGGAAGGATTTGCCCAGGTTTCGCAGAGTCTCGCAGGCTGATCAAAATTCAGCTGCTT	1451			
		481	AAGGCTTGCTCAAGTGAGGTAAATGATGCTCCGAGTCCGCGGACGATACGATCGGCGCTCA	540			
		1452	AAGGCTTGCTCAAGTGAGGTAAATGATGCTCCGAGTCCGCGGACGATACGATCGGCGCTCA	1511			
		541	GACAGTGTCTGTTCGCGAAACAAACGAGCGTACACTCGCGACAACTACCCGCAAGGCTGGC	600			
		1512	GACAGTGTCTGTTCGCGAAACAAACGAGCGTACACTCGCGACAACTACCCGCAAGGCTGGC	1571			
		601	ATGGGCTACGTCATCGAGGATCTACTGCACTTCTGCGCGGTGCATGTACTCTATGGGGTTG	660			
		1572	ATGGGCTACGTCATCGAGGATCTACTGCACTTCTGCGCGGTGCATGTACTCTATGGGGTTG	1631			
		661	GACAAACATCCATTAGCGCTGCTCAACGCGTGTCTGTCATCTTTTCTGACCGCGCCAGGGTTG	720			
		1632	GACAAACATCCATTAGCGCTGCTCAACGCGTGTCTGTCATCTTTTCTGACCGCGCCAGGGTTG	1691			
		721	GAGCAGCGCGCAACTGCGTGGAAAGAAATCCAGCGGTACTACCTGGAATACGCTCCGCACTCAT	780			
		1692	GAGCAGCGCGCAACTGCGTGGAAAGAAATCCAGCGGTACTACCTGGAATACGCTCCGCACTCAT	1751			
		781	ATCCTGAAACACAGTGGCGGGTCCGCGGTTCCGTCGTCATATATACGCGCAAGATCCTCTCA	840			
		1752	ATCCTGAAACACAGTGGCGGGTCCGCGGTTCCGTCGTCATATATACGCGCAAGATCCTCTCA	1811			
		841	ATCCTCTCTGAGCTACGACGCTCGGCGATGCAAAACTCCAACTATGTCATCTCCCTCAAG	900			
		1812	ATCCTCTCTGAGCTACGACGCTCGGCGATGCAAAACTCCAACTATGTCATCTCCCTCAAG	1871			
		901	CTCAAGAACAGAAAAGCTGCGCGCTTTTCTCGAGGAGATCTGGGATGTGGCGGACATGTGCG	960			
		1872	CTCAAGAACAGAAAAGCTGCGCGCTTTTCTCGAGGAGATCTGGGATGTGGCGGACATGTGCG	1931			
		961	CACACCCAAACCGCGCCCTATCTCTGAGTCCCGCAGGATCTCTAGCCCTGCGCGGACGCG	1020			
		1932	CACACCCAAACCGCGCCCTATCTCTGAGTCCCGCAGGATCTCTAGCCCTGCGCGGACGCG	1091			
		1021	ATCGCGGATGCGCGCTCGCGCGCGCTGCTCTGA	1054			
		1992	ATCGCGGATGCGCGCTCGCGCGCGCTGCTCTGA	2025			
RESULT 5							
AX407011							

LOCUS AX407011 1290 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 4 from Patent WO0229075.
ACCESSION AX407011
VERSION AX407011.1 GI:21439858
KEYWORDS
SOURCE Choristoneura fumiferana (spruce budworm)
ORGANISM Choristoneura fumiferana
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Tortricidae; Tortricinae; Choristoneura.
REFERENCE 1
AUTHORS Palli, S.R., Dhaddialla, T.S., Carlson, G.R., Hormann, R.E., Kudla, A.J.,
Mohan, P., Cress, D.E. and Herzig, R.P.
TITLE Multiple inducible gene regulation system
JOURNAL Patent: WO 0229075-A 4 11-APR-2002;
ROHM & HAAS (US)
FEATURES Location/Qualifiers
source
1..1290
/organism="Choristoneura fumiferana"
/mol_type="unassigned DNA"
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ORIGIN

Query Match 97.7%; Score 1029.4; DB 6; Length 1290;
Best Local Similarity 99.7%; Pred. No. 1.7e-238;
Matches 1052; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

QY 1 CCTGAGTGGTGTAGTACCGGAGCTCAGTGGCCCATGAAGCGGAAGAGAAAGACACAG 60
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DB 417 CTCTCCGACAGCTGTTGGAGACAAACCGGACGAAACATCCCTGTTGACAGCCAAC 476
QY 241 CAGCAGTTCCTTATCGCCAGGCTCATCTGTGTACGAGCAGGATACGAGCAGCTTCTGAT 300
DB 477 CAGCAGTTCCTTATCGCCAGGCTCATCTGTGTACGAGCAGGATACGAGCAGCTTCTGAT 536
QY 301 GAAGATTTGAAGAGATTACGACAGCTGTGACGACGAGCGGACGATGAACGAAAGATCT 360
DB 537 GAAGATTTGAAGAGATTACGACAGCTGTGACGACGAGCGGACGATGAACGAAAGATCT 596
QY 361 GACACTCCCTTCGCCAGATCACAGAGATGACTATCCTCAGGTCCTCACTTATCGTGGAG 420
DB 597 GACACTCCCTTCGCCAGATCACAGAGATGACTATCCTCAGGTCCTCACTTATCGTGGAG 656
QY 421 TTCGGAAGGATGTCAGGAGTTCGCCAGGATCTCGAGCCTGATCAAAATACGCTGTT 480
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QY 481 AAGGCTTGCTCAAGTGAAGTAAATGATCTCGAGTTCGCGACGATACGATGCGGCTCA 540
DB 717 AAGGCTTGCTCAAGTGAAGTAAATGATCTCGAGTTCGCGACGATACGATGCGGCTCA 776
QY 541 GACAGTGTCTGTTGGGAAACAAACGAGTACACTCGCGCAACTACCGCAAGGCTGGC 600
DB 777 GACAGTGTCTGTTGGGAAACAAACGAGTACACTCGCGCAACTACCGCAAGGCTGGC 836
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DB 837 ATGGCTACGTCATCGAGGATCTACTGCACTTCTGCGGTCATGATCTATGCGGTTG 896
QY 661 GACAACTCCATTAACGCGCTCTCAACGCGTCTGTCATCTTTTCTGACCGGCTTCTGAT 940

DB 897 GACAACTCCATTAACGCGCTCTCAACGCGTGTGTCATCTTTTCTGACCGGCTTCTGAT 956
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DB 957 GAGCAGCGGCAACTGTGTGGAAGAAATCCAGCGGTACTTACCTGAATAGCTCCGCTAT 1016
QY 781 ATCTGAAACAGCTGAGCGGCTCGGCGGTTCGTCGTCATATATACGGAAGATCTCTCA 840
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QY 841 ATCTCTCTGAGCTAGCAGCTCGGATGCAAACTCCAAACATGTCATCTCCCTCAAG 900
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QY 901 CTCAAGAACAGAAAGCTGCGGCTTTCTCTGAGGAGATCTGGATGTGGC-GGACATGTC 959
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DB 1197 GCACACCAACCGCGCTAT-CTCGAGTCCCCCAAGATCTCTAGCCCTGCGGACAG 1255
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DB 1256 CATCGCGATGCGCGCTCGGCGGCTGCTCTGA 1290

RESULT 6
AX407021
LOCUS AX407021 1073 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 14 from Patent WO0229075.
ACCESSION AX407021
VERSION AX407021.1 GI:21439868
KEYWORDS
SOURCE Choristoneura fumiferana (spruce budworm)
ORGANISM Choristoneura fumiferana
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Tortricidae; Tortricinae; Choristoneura.
REFERENCE 1
AUTHORS Palli, S.R., Dhaddialla, T.S., Carlson, G.R., Hormann, R.E., Kudla, A.J.,
Mohan, P., Cress, D.E. and Herzig, R.P.
TITLE Multiple inducible gene regulation system
JOURNAL Patent: WO 0229075-A 14 11-APR-2002;
ROHM & HAAS (US)
FEATURES Location/Qualifiers
source
1..1073
/organism="Choristoneura fumiferana"
/mol_type="unassigned DNA"
/db_xref="taxon:7141"

ORIGIN

Query Match 95.8%; Score 1010.2; DB 6; Length 1073;
Best Local Similarity 99.2%; Pred. No. 7.6e-234;
Matches 1047; Conservative 0; Mismatches 3; Indels 5; Gaps 3;

QY 1 CCTGAGTGGTGTAGTACCGGAGCTCAGTGGCCCATGAAGCGGAAGAGAAAGACACAG 60
DB 1 CCTGAGTGGTGTAGTACCGGAGCTCAGTGGCCCATGAAGCGGAAGAGAAAGACACAG 60
QY 61 AAGGAGAAGGACAAATGCTGTGACGACGAGCGGTCGACGACGATGCGGCTCAAT 120
DB 61 AAGGAGAAGGACAAATGCTGTGACGACGAGCGGTCGACGACGATGCGGCTCAAT 120
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QY 181 CTCTCCGACAGCTGTTGGAGACAAACCGGACGAAACATCCCTGTTGACAGCCAAC 240
DB 181 CTCTCCGACAGCTGTTGGAGACAAACCGGACGAAACATCCCTGTTGACAGCCAAC 240
QY 241 CAGCAGTTCCTTATCGCAGGCTCATCTGTTGACGAGCGGTCACGAGCAGCTTCTGAT 300

[illegible]

RESULT 7
 AX256354
 LOCUS
 DEFINITION
 Sequence 2 from Patent WO0170816.
 AX256354
 ACCESSION
 VERSION
 AX256354.1 GI:16075205
 KEYWORDS
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 synthetic construct
 synthetic construct
 other sequences; artificial sequences.
 SOURCE
 ORGANISM
 REFERENCE
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 Pali,S.R., Kapitskaya,M.Z. and Cress,D.E.
 Authors
 Ecdysone receptor-based inducible gene expression system
 TITLE
 Patent: WO 0170816-A 2 27-SEP-2001;
 JOURNAL
 ROHM and HAAS COMPANY (US)
 FEATURES
 Location/Qualifiers
 1..1110

Qy 961 CACACCCACCGCGCCTATCTCGAGTCCCGCCAGCAATCTCTAG 1005
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Db 1066 CACACCCACCGCGCCTATCTCGAGTCCCGCCAGCAATCTCTAG 1110
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RESULT 8
AX256401
LOCUS AX256401 1542 bp DNA linear PAT 10-OCT-2001
DEFINITION Sequence 49 from Patent WO0170816.
ACCESSION AX256401
VERSION AX256401.1 GI:16075229
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Palli,S.R., Kapitskaya,M.Z. and Cress,D.E.
TITLE Ecdysone receptor-based inducible gene expression system
JOURNAL Patent: WO 0170816-A 49 27-SEP-2001;
ROHM AND HAAS COMPANY (US)
FEATURES
source
1. .1542
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match 95.4%; Score 1005; DB 6; Length 1542;
Best Local Similarity 100.0%; Pred. No. 1.4e-232;
Matches 1005; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 AAGGAGAAGGCAAACTGCTGTGAGCAGCAGCGGTGAGGAGCAGCATGCCGCCATT 120
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Qy 121 ATGCAGTGTGAACCTCCACCTCTGAGCAGCAAGGATTACAGAGTGGTCCCAAGGTTT 180
Db 658 ATGCAGTGTGAACCTCCACCTCTGAGCAGCAAGGATTACAGAGTGGTCCCAAGGTTT 717
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Qy 181 CTCTCCGACAGCTGTGGAGCAAAACCGGAGCAAAACATCCCGCAGTTGACAGCCAAC 240
Db 718 CTCTCCGACAGCTGTGGAGCAAAACCGGAGCAAAACATCCCGCAGTTGACAGCCAAC 777
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Qy 241 CAGCAGTTCCTTATCGCCAGGCTCATCTGTGACAGGACGGGTACGAGCGCTTCTGAT 300
Db 778 CAGCAGTTCCTTATCGCCAGGCTCATCTGTGACAGGACGGGTACGAGCGCTTCTGAT 837
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Qy 301 GAAGATTGAAGAGGATTACGACAGCTGGCAGCAAGCGGACGATGAAGAGAGTCT 360
Db 838 GAAGATTGAAGAGGATTACGACAGCTGGCAGCAAGCGGACGATGAAGAGAGTCT 897
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Qy 361 GACACTCCCTCCCGCAGATCACAGAGTACTATCTCCAGCGTCCAACTTATCGTGGAG 420
Db 898 GACACTCCCTCCCGCAGATCACAGAGTACTATCTCCAGCGTCCAACTTATCGTGGAG 957
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Qy 421 TTCCGGAAGGATTGCCAGGTTGCCAAGATTCGCAAGCTGTATCAAAATPACGCTGTT 480
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Qy 481 AAGGCTTGCTCAAGTGAAGTAACTGCTCCGAGTCCGCGAGCAGTACGATGCCGCTCA 540
Db 1018 AAGGCTTGCTCAAGTGAAGTAACTGCTCCGAGTCCGCGAGCAGTACGATGCCGCTCA 1077
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Qy 541 GACAGTGTCTGTTCGGGAAACAAACGAGCTACACTCGCGACAACTACCGCAAGGCTGGC 600
Db 1078 GACAGTGTCTGTTCGGGAAACAAACGAGCTACACTCGCGACAACTACCGCAAGGCTGGC 1137
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Qy 601 ATGCGCTACGTCATCGAGGATCTACTGCACTTTCGCGGTGCATGTACTTATCGCGTTG 660
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Db 1138 ATGCGCTACGTCATCGAGGATCTACTGCACTTTCGCGGTGCATGTACTTATGCGCGTTG 1197
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Db 1198 GACAAACATCCATTACGCGCTGCTCAGCGCTGTGCTCATCTTTCTGACCGGCCAGGGTTG 1257
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Qy 721 GAGCAGCGCAACTGTGTGGAAGAAATCCAGCGGTACTACCTGAATACGCTCCGCACTTAT 780
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RESULT 9
AX256357
LOCUS AX256357 960 bp DNA linear PAT 10-OCT-2001
DEFINITION Sequence 5 from Patent WO0170816.
ACCESSION AX256357
VERSION AX256357.1 GI:16075208
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Palli,S.R., Kapitskaya,M.Z. and Cress,D.E.
TITLE Ecdysone receptor-based inducible gene expression system
JOURNAL Patent: WO 0170816-A 5 27-SEP-2001;
ROHM AND HAAS COMPANY (US)
FEATURES
source
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/organism="synthetic construct"
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ORIGIN

Query Match 91.1%; Score 960; DB 6; Length 960;
Best Local Similarity 100.0%; Pred. No. 1.1e-221;
Matches 960; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 AAGGAGAAGGCAAACTGCTGTGAGCAGCAGCGGTGAGGAGCAGCATGCCGCCATT 120
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Qy 121 ATGCAGTGTGAACCTCCACCTCTGAGCAGCAAGGATTACAGAGTGGTCCCAAGGTTT 180
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RESULT 10
AX256414
LOCUS
DEFINITION Sequence 62 from Patent WO0170816.
ACCESSION AX256414
VERSION AX256414.1 GI:16075239
KEYWORDS
SOURCE
ORGANISM
other sequences; artificial sequences.
REFERENCE
AUTHORS Palli,S.R., Kapitskaya,M.Z. and Cress,D.E.
TITLE Ecdysone receptor-based inducible gene expression system
JOURNAL Patent: WO 0170816-A 62 27-SEP-2001;
ROHM AND HAAS COMPANY (US)
FEATURES
source
1. .1247
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ORIGIN
Query Match 88.1%; Score 929; DB 6; Length 1247;
Best Local Similarity 100.0%; Pred. No. 3.6e-214;
Matches 929; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCTGAGTGGTAGTACCGGAGACTCAGTGGCCATGAAGCGGAAAGAGAAAGCACAG 60
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QY 379 AAGGAGAGGACAAACTGCTCTGTCAGACGACGAGCGGTGGACGACCATGTCGCGCCATT 438
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QY 121 ATGCAAGTGAACCTCCACTCTCTGAAGCAGCAAGGATTCAGAAAGTGGTCCCAAGGTTT 180
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QY 439 ATGCAAGTGAACCTCCACTCTCTGAAGCAGCAAGGATTCAGAAAGTGGTCCCAAGGTTT 498
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QY 181 CTCTCCGACACAGCTGTTGGAGACAAACCGGCGAGAAAAAATCATCCCCAGTTGACAGCAAC 240
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QY 499 CTCTCCGACACAGCTGTTGGAGACAAACCGGCGAGAAAAAATCATCCCCAGTTGACAGCAAC 558
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QY 241 CAGCAGTTCCTTATGCGCAGGCTCATCTGTTACGAGGACGGGTACGAGCAGGCTTCTGAT 300
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QY 301 GAAGATTTTGAAGAGGATTAACGACAGCTGGCAGCAAGCGGACGATGAAACGAAAGTCT 360
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QY 721 GAGCAGCGCAACTGTTGGGAAGAAATCCAGCGGTACTTACCTGAATAGCTCCGCACTAT 780
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QY 901 CTCGAAGAACAGAGCTGCGCCCTTCTCAGAGAGATCTGGATGTGGCGGACATGTGCG 929
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DB |||||||

RESULT 11
AX256356
LOCUS
DEFINITION Sequence 4 from Patent WO0170816.
ACCESSION AX256356
VERSION AX256356.1 GI:16075207
KEYWORDS
SOURCE
ORGANISM
other sequences; artificial sequences.
QY 901 CTCGAAGAACAGAGCTGCGCCCTTCTCAGAGAGATCTGGATGTGGCGGACATGTGCG 929
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QY 1219 CTCGAAGAACAGAGCTGCGCCCTTCTCAGAGAGATCTGGATGTGGCGGACATGTGCG 1247
DB |||||||
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REFERENCE
AUTHORS Palli,S.R., Kapitskaya,M.Z. and Cress,D.E.
TITLE Ecdysone receptor-based inducible gene expression system
JOURNAL Patent: WO 0170816-A 4 (27-SEP-2001;
ROHM AND HAAS COMPANY (US))
FEATURES
source Location/Qualifiers
1..735 /organism="synthetic construct"
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ORIGIN

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Best Local Similarity	100.0%;	Pred. No. 3.7e-167;		
Matches 735;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

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QY      271   TACCAGGACGGGTACGAGCAGCGCTTCTGATGAAGATTGAAAGAGATTACGCAGACTGG    330
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Db       1     TACCAGGACGGGTACGAGCAGCGCTTCTGATGAAGATTGAAAGAGATTACGCAGACTGG    60

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QY      451   ATCTCGCAGCGCTGATCAAATTAAGCTCTTAAGGCTTGTCAAGTGAGGTAATGATGCTC    510
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QY      511   CGAGTTCGCGGACGATACGATGCGGCTCTCAGACAGTGTTCCTGTCGCGAACAACAAGCG    570
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RESULT 12
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DEFINITION Plodia interpunctella ecdysone receptor mRNA, complete cds.

ACCESSION	AY489269	2	GI:45827647	
VERSION	AY489269.2			
KEYWORDS				
SOURCE	Plodia interpunctella (Indianmeal moth)			
ORGANISM	Plodia interpunctella			
	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Pyraloidea; Pyralidae; Phycitinae; Plodia.			
REFERENCE	1 (bases 1 to 6083)			
AUTHORS	Slausat,D., Bozzolan,F., Queguiner,I., Porcheron,P. and Debernard,S.			
TITLE	Effects of juvenile hormone on 20-hydroxyecdysone-inducible EcR, HR3, E75 gene expression in imaginal wing cells of Plodia interpunctella lepidoptera			
JOURNAL	Eur. J. Biochem. 271 (14), 3017-3027 (2004)			
PUBMED	15233798			
REFERENCE	2 (bases 1 to 6083)			
AUTHORS	Slausat,D., Debernard,S., Bozzolan,F., Queguiner,I. and Porcheron,P.			
TITLE	Direct Submission			
JOURNAL	Submitted (28-NOV-2003) Laboratoire De Physiologie Cellulaire Des Invertebres, Universite Pierre Et Marie Curie, 12 Rue Cuvier, Paris 75005, France			
REFERENCE	3 (bases 1 to 6083)			
AUTHORS	Slausat,D., Debernard,S., Bozzolan,F., Queguiner,I. and Porcheron,P.			
TITLE	Direct Submission			
JOURNAL	Submitted (30-MAR-2004) Laboratoire De Physiologie Cellulaire Des Invertebres, Universite Pierre Et Marie Curie, 12 Rue Cuvier, Paris 75005, France			
REMARK	Sequence update by submitter			
COMMENT	On Mar 30, 2004 this sequence version replaced gi:40362585.			
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CDS				
	64.9%; Score 683.6; DB 2; Length 6083;			
	Best Local Similarity 80.3%; Pred. No. 1.1e-154;			
	Matches 816; Conservative 0; Mismatches 194; Indels 6; Gaps 1;			
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Qy	61	AAGGAGAGGACAAACTGCTGTGCAGCAGCAGCGGTGGACGACCACCATGCCGCCCATTT	120	
Db	1072	AGGGAGAAAGACAAATTTGCCCGTGAGCAGCAGCAGTCGACCATCATGCCCCCCCNTC	1131	
Qy	121	ATGCAGTGTGAACCTCCACCTCTCGAAGCAGCAGGATTCCAGAGTGGTCCCAAGGTTT	180	
Db	1132	ATGCAGTGCATCGGCCACACACAGAGCGCGCCAGGATTCACGAGTGGTCCCGCGGTTT	1191	
Qy	181	CTTCCGACAAAGCTGTTGGAGACAAACCCGCGAGAAAACATGCCCATGTTGACAGCAAC	240	


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Db      2009  CCCCCGCCACGCGATCGCGCGCTCGCGCGCGCCCGCGCGC 2050

RESULT 15
LOCUS   AR274109
DEFINITION Sequence 1 from patent US 6504082.
ACCESSION AR274109
VERSION   AR274109.1 GI:29706084
KEYWORDS .
SOURCE   Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2126)
AUTHORS  Albertsen,M.C., Brooke,C.D., Garnaat,C.W. and Roth,B.A.
TITLE    Ecdysone receptors and methods for their use
JOURNAL  Patent: US 6504082-A 1 07-JAN-2003;
        Pioneer Hi-Bred International, Inc.; Des Moines, IA
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Best Local Similarity 76.6%; Pred. No. 2:9e-143;
Matches 813; Conservative 0; Mismatches 231; Indels 18; Gaps 2;

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Qy      121  ATGCAGTGTGAACCTCCACCTCTCTGAGCAGCAGGATT-----CAGGAA 165
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Qy      166  GTGTCTCCAAAGGTTTCTCTCCGACAAGCTGTGTGGAGACAACCGGCGAGAAACATCCCC 225
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Qy      226  CAGTTGACAGCAACACGAGTTCCTTAATGCCAGGCTCATCTGTTACCGAGGCGGTAC 285
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Qy      286  GAGCAGCTTCTGATGAAGATTGTAAGAGGATTAACGAGACTGCGAGCAAGCGGACGAT 345
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Qy      346  GAAAGCAAGAGTCTGACACTCCCTTCGCGCAGATCAAGAGATGACTATCCTCACGGTC 405
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Qy      406  CAACCTATCTGGAGTTGCGAGGGATTCGAGGGTTTCGCAAGATCTCGAGCCTGAT 465
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Qy      466  CAAATTACGCTGCTTAAGGCTTGTCTCAAGTGAAGTATGATGCTCCGAGTCGCGCAGCA 525
Db      1469  CAGATCAATATTAAAGGCAATGCTCAAGGAGTGAATGATGCTCCGAGTAGCGAGCGG 1528

Qy      526  TACGATCGGCTCAGACAGTGTCTGTTCGCGAACCAACCAAGCGTACACTTCGCGACAAC 585
Db      1529  TACGACGGGTGTCGGATAGCGTTCTGTTCGCCCAACCAACAGGGGTACACTTCGCGACAAC 1588

Qy      586  TACGCAAGGCTGGCATGGCTACGTATCAGAGATCTATCTGCACTTCTGCGCGGTGATG 645
Db      1589  TACGCAAGGCGGCGATGGCGTACGTATCAGAGACCTGTGTGCACTTCTGCGCGTGCATG 1648

Qy      646  TACTCTATGGGTTGGACAAACATCCATTACGGGCTGTCTACGGGCTGTCTCTTCT 705

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Db      1649  TACTGATGTCGATGGACAAAGTGTATTACGGCTCTCTCAGTCCTGATGTTATTTCTCG 1708

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Qy      766  AGCTCCGCGATCTATATCTCTGAACCGAGCTGAGCGGGTGGCGGGTTCGTCCTCATATAC 825
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Qy      826  GCAAGATCTCTCAATCTCTCTGAGCTACGACGCTCGGATGCAAACTCCCAACATG 885
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Qy      886  TGCATCTCCCTCAAGCTCAAGAACAGAAAGCTGCGCCCTTTCTCTGAGAGATCTGGGAT 945
Db      1889  TGCATCTCGCTGAAGCTCAAGAACAGAAAGCTGCGCCGCTTCTCTGAGAGATTTGGGAC 1948

Qy      946  GTGGGGGACATGTGCGACACCCCAACCGCGCGCTATCTCTGAGTCCCGCAGCAATCTCTAG 1005
Db      1949  GTGGCGGACGTGTGCGACGCGCGCGCTGTGTGGCGGACGCGGCTACGGGCTCTAG 2008

Qy      1006  CC---CCTGCGCGCACGCGATCGCGTCCGCGCGC 1044
Db      2009  CCGCGCCACGCGATCGCGCGCGCTCGCGCGCGCGCGCGC 2050

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result#	Nc#	Score	Query Match	Length	DB ID	Description
1	1001.8	95.0	1008	8	US-11-118-855-21	Sequence 21, Appl
2	961.2	91.2	2595	6	US-10-888-613B-93	Sequence 93, Appl
3	330.6	31.4	2241	6	US-10-828-831-4	Sequence 4, Appl
4	330.6	31.4	2241	6	US-10-828-831-6	Sequence 6, Appl
5	330.6	31.4	3126	6	US-10-828-831-8	Sequence 8, Appl
6	125.4	11.9	1383	8	US-11-076-163-6	Sequence 6, Appl
7	125.4	11.9	1959	8	US-11-136-527-2980	Sequence 2980, Appl
8	125.4	11.9	2033	8	US-11-166-412-18	Sequence 18, Appl
9	94.4	9.0	1344	8	US-11-076-163-2	Sequence 2, Appl
10	94.4	9.0	1528	8	US-11-166-412-2	Sequence 2, Appl
11	75.8	7.2	2156	8	US-11-136-527-2936	Sequence 2936, Appl
12	74	7.0	2329	8	US-11-136-527-1966	Sequence 1966, Appl
13	67.6	6.4	2355	8	US-11-112-908-15	Sequence 15, Appl
14	66.2	6.3	1400	8	US-11-136-527-4435	Sequence 4435, Appl
15	66.2	6.3	1723	8	US-11-136-527-339	Sequence 339, Appl
16	61.2	5.8	1775	8	US-11-136-527-4037	Sequence 4037, Appl
17	56.4	5.4	4550	8	US-11-136-527-1874	Sequence 1874, Appl
18	54.2	5.1	2043	8	US-11-136-527-2325	Sequence 2325, Appl
19	53.6	5.1	3119	8	US-11-000-688-398	Sequence 398, Appl
20	50.4	4.8	3923	8	US-11-136-527-3450	Sequence 3450, Appl
21	45.4	4.3	600	8	US-11-136-527-7076	Sequence 7076, Appl
22	45.2	4.3	2007	8	US-11-136-527-1897	Sequence 1897, Appl

23	44.4	4.2	1400	8	US-11-136-527-7923	Sequence 7923, Ap
24	44.4	4.2	2070	8	US-11-136-527-3827	Sequence 3827, Ap
25	44.4	4.2	3518	8	US-11-136-527-2799	Sequence 2799, Ap
26	42.2	4.0	2130	8	US-11-136-527-2138	Sequence 2138, Ap
27	41	3.9	600	8	US-11-136-527-4470	Sequence 4470, Ap
c 28	41	3.9	852	8	US-11-136-527-374	Sequence 374, App
29	40.4	3.8	806	8	US-11-112-908-398	Sequence 398, App
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31	40.4	3.8	161994	8	US-11-112-908-57	Sequence 57, Appl
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33	40.4	3.8	168656	8	US-11-112-908-59	Sequence 59, Appl
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35	40.4	3.8	170285	8	US-11-112-908-58	Sequence 58, Appl
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ALIGNMENTS

RESULT 1

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; Sequence 21, Application US/11118855
; Publication No. US20050266457A1
; GENERAL INFORMATION:
; APPLICANT: Palli, Subba Reddy
; APPLICANT: Kumar, Mohan
; TITLE OF INVENTION: Mutant Receptors and Their Use in a Nuclear Receptor-Based
; FILE REFERENCE: A01508-US
; CURRENT APPLICATION NUMBER: US/11/118,855
; CURRENT FILING DATE: 2005-04-28
; PRIOR FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: US 60/567,294
; PRIOR FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 60/609,424
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21
; LENGTH: 1008
; TYPE: DNA
; ORGANISM: Choriostoneura fumiferana
US-11-118-855-21

Query Match 95.0%; Score 1001.8; DB 8; Length 1008;
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Matches 1003; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 244 CAGCAGTTCCTTATGTCAGGCTCATCTGTTACAGGAGCGGTACAGCAGCCTTCTGAT 303
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Db 304 GAAGATTGGAAGGATTACGAGAGCTGCGAGAGCGGAGCGGAGATGAAACGAAGAGTCT 363
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Qy 421 TTGCGGAAGGATTGCGCAGGTTGCGCAAGATCTGCGAGCCTGATCAAAATTAAGCTGCTT 480
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Qy 481 AAGGCTTGCTCAAGTAGGTAATGATGCTCCGAGTCCGCGAGATACGATGCGGCTCA 540
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Qy 961 CACACCCAAACGCGGCTTCTCGAGTCCGCCCAAGATCTCTAG 1005
Db 964 CACACCCAAACGCGGCTTCTCGAGTCCGCCCAAGATCTCTAG 1008

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RESULT 2
US-10-888-613B-93
; Sequence 93, Application US/10888613B
; Publication No. US20060008911A1
; GENERAL INFORMATION:
; APPLICANT: Donald Danforth Plant Science Center
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REGULATING GENE EXPRESSION IN PLANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 0104850
; CURRENT APPLICATION NUMBER: US/10/888,613B
; CURRENT FILING DATE: 2004-07-09
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 93
; LENGTH: 2595
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: This sequence was artificially derived and/or created by the
; OTHER INFORMATION: inventors.
US-10-888-613B-93

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Query Match 91.2%; Score 961.2; DB 6; Length 2595;
Best Local Similarity 99.2%; Pred. No. 1.2e-260;
Matches 998; Conservative 0; Mismatches 3; Indels 5; Gaps 3;
Qy 1 CTTGAGTGGTGTAGTACCCGAGAGCTCAGTGGCGCATGGAAGCGGAAAGAGAAAGACACAG 60
Db 751 CTTGAGTGGTGTAGTACCCGAGAGCTCAGTGGCGCATGGAAGCGGAAAGAGAAAGACACAG 810
Qy 61 AAGGAGAAGGACAAACTGCTCTGTACGACGACGAGCGGTGGAGCAGACCATGCGGCCCATTT 120
Db 811 AAGGAGAAGGACAAACTGCTCTGTACGACGACGAGCGGTGGAGCAGACCATGCGGCCCATTT 870
Qy 121 ATGCACTGTGAACCTTCACTCTGAGCAGCAGCAAGGATTCACGAGTGGTCCCAAGGTTT 180
Db 871 ATGCACTGTGAACCTTCACTCTGAGCAGCAGCAAGGATTCACGAGTGGTCCCAAGGTTT 930
Qy 181 CTCTCCGACAAAGCTGTTGGAGACAAACCGCGAGAAAAACATCCCCAGTTTGACAGCAAC 240
Db 931 CTCTCCGACAAAGCTGTTGGAGACAAACCGCGAGAAAAACATCCCCAGTTTGACAGCAAC 990
Qy 241 CAGCAGTTCCTTATCGCCAGGCTCATCTGTTACGAGCAGCGGTACGAGCAGCCTTCTGAT 300
Db 991 CAGCAGTTCCTTATCGCCAGGCTCATCTGTTACGAGCAGCGGTACGAGCAGCCTTCTGAT 1050
Qy 301 GAAGATTGGAAGGATTACGAGAGCTGCGAGCAGCGGAGCGGAGATGAAACGAAGAGTCT 360
Db 1051 GAAGATTGGAAGGATTACGAGAGCTGCGAGCAGCGGAGCGGAGATGAAACGAAGAGTCT 1110
Qy 361 GACACTCCCTTCGCGCAGATACAGAGATGACTATCTCAGCGTCCAACTTATGCTGGAG 420
Db 1111 GACACTCCCTTCGCGCAGATACAGAGATGACTATCTCAGCGTCCAACTTATGCTGGAG 1170
Qy 421 TTGCGGAAGGATTGCGCAGGTTGCGCAAGATCTCGCAGCCTGATCAAAATTAAGCTGCTT 480
Db 1171 TTGCGGAAGGATTGCGCAGGTTGCGCAAGATCTCGCAGCCTGATCAAAATTAAGCTGCTT 1230
Qy 481 AAGGCTTGCTCAAGTAGGTAATGATGCTCCGAGTCCGCGAGCGGATACGATGCGGCTCA 540
Db 1231 AAGGCTTGCTCAAGTAGGTAATGATGCTCCGAGTCCGCGAGCGGATACGATGCGGCTCA 1287
Qy 541 GACAGTGTCTGTTGCGGAACCAACCAAGCGTACACTCGCGACAACTACCGCAAGGCTGGC 600
Db 1288 GACAGTGTCTGTTGCGGAACCAACCAAGCGTACACTCGCGACAACTACCGCAAGGCTGGC 1347
Qy 601 ATGGCCTTACGTCATCGAGGATCTACTGCACTTCTGCGGCTGCACTCTATGCGGTTG 660
Db 1348 ATGGCCTTACGTCATCGAGGATCTACTGCACTTCTGCGGCTGCACTCTATGCGGTTG 1407
Qy 661 GACAACTCATTAACGCGCTGCTCAGCGGCTGCTCATCTGAGCAGCGGAGTCTCTAG 720
Db 1408 GACAACTCATTAACGCGCTGCTCAGCGGCTGCTCATCTGAGCAGCGGAGTCTCTAG 1467
Qy 721 GAGCAGCGCAACTGCTGGGAAGAAATCCAGCGGTACTACTGAATACGCTCCGATCTAT 780
Db 1468 GAGCAGCGCAACTGCTGGGAAGAAATCCAGCGGTACTACTGAATACGCTCCGATCTAT 1527
Qy 781 ATCTGAAACAGCTGAGCGGCTGCGGCGGTTGTCGTCATATACGCGCAAGATCTCTCA 840
Db 1528 ATCTGAAACAGCTGAGCGGCTGCGGCGGTTGTCGTCATATACGCGCAAGATCTCTCA 1587
Qy 841 ATCTCTCTGAGCTACGAGCCTGCGGATGCAAACTCCAACTATGTCATCTCCCTCAAG 900
Db 1588 ATCTCTCTGAGCTACGAGCCTGCGGATGCAAACTCCAACTATGTCATCTCCCTCAAG 1647
Qy 901 CTCAAGAACAGAAAGCTGCGGCTTCTCGAGGAGATCTGGGATGTCGGG-GGACATGTC 959
Db 1648 CTCAAGAACAGAAAGCTGCGGCTTCTCGAGGAGATCTGGGATGTCGGGAGACATGTC 1707
Qy 960 GCAACCCAAACCGCGCTTATCTCGAGTCCGCCCAAGATCTCTAG 1005
Db 1708 GCAACCCAAACCGCGCTTAT-CTCGAGTCCGCCCAAGATCTCTAG 1752

```

RESULT 3

US-10-828-831-4
; Sequence 4, Application US/10828831
; Publication No. US20060014711A1
; GENERAL INFORMATION:
; APPLICANT: EVANS, RONALD M.
; APPLICANT: NO, DAVID
; APPLICANT: SAEZ, ENRIQUE
; TITLE OF INVENTION: METHODS FOR MODULATING EXPRESSION OF EXOGENOUS GENES IN
; FILE REFERENCE: SALK1520-2
; CURRENT APPLICATION NUMBER: US/10/828,831
; CURRENT FILING DATE: 2004-04-20
; PRIOR APPLICATION NUMBER: US/09/042,488
; PRIOR FILING DATE: 1998-03-16
; PRIOR APPLICATION NUMBER: 08/974,530
; PRIOR FILING DATE: 1997-11-19
; PRIOR APPLICATION NUMBER: 08/628,830
; PRIOR FILING DATE: 1996-04-05
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 2241
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Recombinant
; OTHER INFORMATION: VgEcr
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2238)
US-10-828-831-4

Query Match 31.4%; Score 330.6; DB 6; Length 2241;
Best Local Similarity 59.5%; Pred. No. 4.1e-83;
Matches 617; Conservative 0; Mismatches 384; Indels 36; Gaps 2;

Qy	1	CCTGAGTGCCTAGTACCCGAGACTCAGTGCCTCCATGAAGCGGAAAGAGAAAGACAG	60
Db	595	CCGGAATGGTCTGCTCCGAGAACCAATGTGGATGAAGCGCGGAAAGAGGCCAG	654
Qy	61	AAGAGAAGGACAACTGCTGTGAGCAGACGAGCGTGGAGACCAATGCCGCCATT	120
Db	655	AAGAGAAGGACAAATGACCACTTCGCCAGCTCTCAGCATGCGCGCAATGGCAGCTT	714
Qy	121	ATGCAAGTGTGAACCTCCACTCTGAGCAGCAGGATTCAGAGTGGTCCAG----	176
Db	715	GCCTCTGTGGCGGCCAAGACTTTGTTAAGAAGAGAGATTCTTGACCTTATGACATGCGAG	774
Qy	177	-----GTTTCTCTCCGACAACTGTTGGAGACAAACCGGCAG	213
Db	775	CGCCCCCAGCATGCCACTATTCGCTACTCTGATGAATATTTGGCCAGTGTCAAGCG	834
Qy	214	AAAAACATCCCCAGTTGAGCAACCAAGCAGTTCTTATCGCAGGCTCATCTGGTAC	273
Db	835	CGCAATATACCTCTTAAACGTACAACTCAGTTGGCCGTTATATACAAAGTTAAATTTGGTAC	894
Qy	274	CAGACGGGTACGAGCAGCTCTGATGAAGATTGAGAGGATTACGACAGCTGGCAG	333
Db	895	CAGATGGCTATGAGCAGCCATCTGAAGAGGATCTCAGGCGTAAATGAGT-----	945
Qy	334	CAAGCGGACGATGAAGAGAGTCTGACACTCCCTTCGCCAGATCAGAGATGACT	393
Db	946	CAACCCGATGAGACGAGGACCAACGAGCTGAGCTTTCGGCATATACCGAGATACC	1005
Qy	394	ATCTCAAGTCCAACTTATCGTGGAGTTCCGAGGAGTTGCCAGGTTCCGCAAGATC	453
Db	1006	ATACTCAGGTCAGTTGATTTGTTGAGTTTCTAAAGGTCTACCAAGGTTTACAAAGATA	1065
Qy	454	TCGAGGCTGATCAATTAACGCTTTAAGGCTTCTCAAGTGAAGTAAATGATGCTCGA	513
Db	1066	CCCCAGGAGGACCAAGATCAAGCTTAAAGGCTGCTCGTGGAGGTGATGATGCTGCGT	1125

Qy	514	GTCCGCGACGATACGATCGCGCTCAGACAGTGTCTGTTCGGAACAAACAGCGTAC	573
Db	1126	ATGGCAGCAGCTATGACCAAGCTCGGACTCAATATTTCTTCGGAATAATAGATCAT	1185
Qy	574	ACTCGGACAACTACCGCAAGGCTGGCATGGCCCTACGTATCAGGAGTCTACTGCACTTC	633
Db	1186	ACGCGGATTTCTTACAAATATGGCCGAATGGCTGATTAACATTTGAAGACCTCTGCAATTC	1245
Qy	634	TGCCGCTGATGTACTCTATGGCGTTGGACAAACATCAATATACGCGCTGCTCAGCGCTGC	693
Db	1246	TGCCGCCAATTTCTTCTGATGAAGTGGACAACTCGAATACGCGCTTCTCACTGCGCAAT	1305
Qy	694	GTCACTCTTTTGTGACCGGCCAGGGTTGGAGCAGCCGCAACTGTGGTGAAGAAATCCAGCG	753
Db	1306	GTGATCTTCTCGGACCGCGCGGCTGGAGAAGGCCCACTAGTCTGAAGCGATCCAGAGC	1365
Qy	754	TACTACTGATATACGCTCCGATCTATATCTGAACAGCTGAGCGGGTGGCGGTTGCG	813
Db	1366	TACTACATCGACACGCTACGCAATTTATATCTCAACGCCCACTCGCGCGACTCAATGAGC	1425
Qy	814	TCCGTATATACGCAAGATCTCTCAATCTCTCTGAGCTACGACGCTCGGATGCAA	873
Db	1426	CTGCTCTTACGCAAGAGTGTCTCTCGATCTCTACCGAGCTCGTAGCTGGGCAACG	1485
Qy	874	AATCCAACTGTGCTCTCTCAAGCTCAAGAACAGAAAGTGCCTCTTCTCTCGAG	933
Db	1486	AAGCCGAGATGTGTTCTCACTAAAGCTCAAAACCGCAACTGCCCAAGTCTCTCGAG	1545
Qy	934	GAGATCTGGATGGCGGACATGTCCGACACCCCAACCGCGGCTATCTCGAGTCCCCC	993
Db	1546	GAGATCTGGGAGCTTCATGCCATCCGCCATCGGTCCAGTCCGACCTTCAGATTACCCAG	1605
Qy	994	ACGAATCTTAGCCCT 1010	
Db	1606	GAGGAGAACGAGCGTCT 1622	

RESULT 4

US-10-828-831-6
; Sequence 6, Application US/10828831
; Publication No. US20060014711A1
; GENERAL INFORMATION:
; APPLICANT: EVANS, RONALD M.
; APPLICANT: NO, DAVID
; APPLICANT: SAEZ, ENRIQUE
; TITLE OF INVENTION: METHODS FOR MODULATING EXPRESSION OF EXOGENOUS GENES IN
; FILE REFERENCE: SALK1520-2
; CURRENT APPLICATION NUMBER: US/10/828,831
; CURRENT FILING DATE: 2004-04-20
; PRIOR APPLICATION NUMBER: US/09/042,488
; PRIOR FILING DATE: 1998-03-16
; PRIOR APPLICATION NUMBER: 08/974,530
; PRIOR FILING DATE: 1997-11-19
; PRIOR APPLICATION NUMBER: 08/628,830
; PRIOR FILING DATE: 1996-04-05
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 2241
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Recombinant
; OTHER INFORMATION: VpEcr
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2238)
US-10-828-831-6

Query Match 31.4%; Score 330.6; DB 6; Length 2241;
Best Local Similarity 59.5%; Pred. No. 4.1e-83;

Db 1951 CCCAGGAGGACAGATCAGTTACTAAAGGCTCTGTCGCGAGGTGATGATGCTGCGT 2010
 Qy 514 GTGCGCGCAGATAGATGCGGCTCAGACAGTGTCTGTTGCGCAACAAACCAACGCTAC 573
 Db 2011 ATGGCAGCAGGCTATGACACACAGCTCGACTCAATATTCTTCGCGAATAATAGATCAT 2070
 Qy 574 ACTCGCGCACTACCGCAGGCTGCGATGGCTAGCTCATCGAGGATCTACTGCACTTC 633
 Db 2071 ACGCGGGAATCTTACAAAATGSCCGGAATGGCTGATTAACATTAAGAGACCTGCTGCAATTC 2130
 Qy 634 TSCCGGTGATGATCTCTATGSCGTTGGACACATCCATTACGCGCTGCTCAGCGCTGC 693
 Db 2131 TGCCGCCAAATGTTCTCGATGAAGTGGACACGTCGAATACGCGCTTCTCACTGCCATT 2190
 Qy 694 GTCACTTTTTCGACCGGCGAGGTTGGAGCAGCGCCAACTGGTGGAAAGAAATCCAGCGG 753
 Db 2191 GTGATCTTCTCGGACCGGCGGCTGAGAGAGGCCCACTAGTTCGAAGCGATCCAGAGC 2250
 Qy 754 TACTACCTGAATACGCTCGCATCTATATCTGAACAGCTAGCGGGTGGCGGCTTCG 813
 Db 2251 TACTACATCGACACGCTAGCATTTATATATCTCAACCGCCACTGCGGCGACTCAATGAGC 2310
 Qy 814 TCCGTCATATAGCGCAAGATCTCTCAATCTCTGAGCTACGACGCTCGGCAATGCAA 873
 Db 2311 CTGCTCTTCTAGCAAGCTGCTCTCGATCTCTCAACCGCTGCTGAGCTGCGTACGCTGCGCAACCG 2370
 Qy 874 AACTCCAACTGTGATCTCCCTCAAGCTCAAGAAACAGAAAGCTCCGCGCTTTCTCCGAG 933
 Db 2371 AAGCGCGAGTGTGTTCTCACTAAGCTCAAAACCGCAACTGCCCAAGTTCCTCGAG 2430
 Qy 934 GAGATCTGGATGTGGCGACATGTGCGACACCCCAACCGCGCTTATCTCGAGTCCGCC 993
 Db 2431 GAGATCTGGAGCTTCATGCCATCCGCGCATCGGTCCAGTCCGACCTTCAGATTACCCAG 2490
 Qy 994 ACGAATCTTAGCCCT 1010
 Db 2491 GAGGAGACGAGCGTCT 2507
 RESULT 6
 US-11-076-163-6
 ; Sequence 6, Application US/11076163
 ; Publication No. US20050261319A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Deuschle, Ulrich
 ; APPLICANT: Loebbert, Ralph
 ; APPLICANT: Blume, Beatrix
 ; APPLICANT: Koegi, Manfred
 ; APPLICANT: Kremoser, Claus
 ; APPLICANT: Kober, Ingo
 ; APPLICANT: Bauer, Ulrike
 ; APPLICANT: Hermann, Kristina
 ; APPLICANT: Albers, Michael
 ; TITLE OF INVENTION: Novel 2-amino-4-quinazolinones and 2-amino-4-oxoquinazolinones as
 ; TITLE OF INVENTION: LXR Nuclear Receptor Binding Compounds with Partial Agonistic
 ; TITLE OF INVENTION: Properties
 ; FILE REFERENCE: BB-139
 ; CURRENT APPLICATION NUMBER: US/11/076,163
 ; CURRENT FILING DATE: 2005-03-09
 ; PRIOR APPLICATION NUMBER: PCT/EP03/10036
 ; PRIOR FILING DATE: 2003-09-10
 ; PRIOR APPLICATION NUMBER: PCT/EP03/07067
 ; PRIOR FILING DATE: 2003-07-02
 ; PRIOR APPLICATION NUMBER: EP 02020255.2
 ; PRIOR FILING DATE: 2002-09-10
 ; NUMBER OF SEQ ID NOS: 9
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 6
 ; TYPE: DNA
 ; LENGTH: 1383
 ; ORGANISM: Homo sapiens
 US-11-076-163-6

Query Match 11.9%; Score 125.4; DB 8; Length 1383;
 Best Local Similarity 54.7%; Pred. No. 2e-25;
 Matches 321; Conservative 0; Mismatches 251; Indels 15; Gaps 3;
 Qy 367 CCCTTCGCCAGATCAGAGATGACTATCTCAGGTCGAACTTATCTGAGGTTCCGG 426
 Db 796 CGCTTTCGCCACTTCAAGGAGCTGGCCATCATCTCAGTCCAGGAGATCGTGGACTTCGCT 855
 Qy 427 AAGGAGATTGCCAGGTTGCGCAAGATCTCGCAGCTGATCAAAATTACGCTGCTTAAGGCT 486
 Db 856 AAGCAAGTGCCTGTTCTCTCAGCTGGGCGGAGGACGAGATCGCCTCTCTGAGGCA 915
 Qy 487 TGCTCAAGTAGGTAATGATGCTCCGAGTCGCGCGAGATACGATGCGGCTCTCAGACAGT 546
 Db 916 TCCACTATCGAGATCATCTGCTAGAGACAGCCAGGCGCTACAAACCAACGACAGAGTGT 975
 Qy 547 GTTCTGTTGGCGAACAACCAAGCTGACTCGCGACCACTACCGCAACTACCGCAAGCTGGCAT---G 603
 Db 976 ATCACTTCTTGAAGGACTTCACTACGAGCAAGGACGACTTCCACCGTGCAGGCTTCGAG 1035
 Qy 604 GCCTACGCTCATCGAGGATCTACTGCACATTCTGCGGCTGCTACTCTATGCGCTGGAC 663
 Db 1036 GTGGAGTTCAATACCCCATCTTCGAGTTCTCGCGGCGCATGCGGCGCTGGGCTGGAC 1095
 Qy 664 AACTTCATTAACGCTGCTCAGCGCTGTGTCATCTTTT---CTGACCGGCCAGGGTTG 720
 Db 1096 GACGCTGAGTACGCGCTGCTCATCGCATCAACATCTTCTCGGCGCAGCCGCGCCCAACGCTG 1155
 Qy 721 GAGCAGCGCAACTGCTGGAGAAATCCAGCGCTACTACCTGGAATAGCTCCGCTCAT 780
 Db 1156 CAGAGCGCGGCGCGCTGGAGGCGTTGCGAGCAGCCCTACGTTGGAGGCGCTCTGTCTTAC 1215
 Qy 781 ATCTGTAACACAGCTGAGCGGCTCGCGCTGCTGCTCATATACGCGCAAGATCTCTCA 840
 Db 1216 ACGCGCATCAAGA-----GCGCGAGACAGCTGCGCTTCCGCGCATGCTCATG 1266
 Qy 841 ATCTCTCTGAGCTACGACGCTCGCATGCGCAATGCAAACTCCAAATGTGCTATCTCCCTCAAG 900
 Db 1267 AAGCTGTGAGCTGCGCAGCTGAGCTCTGTGCACTCGGAGCAGGTCTTTCGCTTGGCGG 1326
 Qy 901 CTCGAAGACAGAAAGCTGCGGCTTCTCTCGAGGAGATCTGGGATGT 947
 Db 1327 CTCGAGCAAGAAAGCTGCGGCTTCTCTGCTGTGCGAGATCTGGGACGT 1373
 RESULT 7
 US-11-136-527-2980
 ; Sequence 2980, Application US/11136527
 ; Publication No. US20050287570A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wyeth
 ; APPLICANT: Mounts, William M
 ; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
 ; FILE REFERENCE: 031896-041000 (AM101086)
 ; CURRENT APPLICATION NUMBER: US/11/136,527
 ; CURRENT FILING DATE: 2005-05-25
 ; PRIOR APPLICATION NUMBER: US 60/574,294
 ; PRIOR FILING DATE: 2005-05-26
 ; NUMBER OF SEQ ID NOS: 362830
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 2980
 ; LENGTH: 1959
 ; TYPE: DNA
 ; ORGANISM: Rattus norvegicus
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (1899)..(1899)
 ; OTHER INFORMATION: n is a, c, g, or t
 US-11-136-527-2980
 Query Match 11.9%; Score 125.4; DB 8; Length 1959;
 Best Local Similarity 46.7%; Pred. No. 2.3e-25;
 Matches 364; Conservative 49; Mismatches 348; Indels 18; Gaps 4;

; PRIOR APPLICATION NUMBER: PCT/EP03/07067
 ; PRIOR FILING DATE: 2003-07-02
 ; PRIOR APPLICATION NUMBER: EP 02020255.2
 ; PRIOR FILING DATE: 2002-09-10
 ; NUMBER OF SEQ ID NOS: 9
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 2
 ; LENGTH: 1344
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-11-076-163-2

Query Match 9.0%; Score 94.4; DB 8; Length 1344;
 Best Local Similarity 49.3%; Pred. No. 1e-16;
 Matches 369; Conservative 0; Mismatches 361; Indels 18; Gaps 4;

Qy	215	AAAAATCCCCCAGTGTGACAGCCCAACAGAGTTCCTTATCGCCAGGCTCATCTGTATCC	274
Db	602	AAATCTCTGCCCACTGAGCCCGGAACACTGGGCATGATCGAAGCTCTGCTGCTGCC	661
Qy	275	AGGACGGGTACGAGCAGCTTCTGATGAAGATTTGAAGAGATTTACGACAGCTGGCAGC	334
Db	662	AGCAACAGTGAACCGGGCTCTTCTGACCGGCTTCGAGTCAAGCTTGGGCCATGG	721
Qy	335	AAGCGAGCATGAAGAAACGAAGATC---TGACATCTCCCTTCGCGCAGATCAAGATGA	391
Db	722	CACAGATCTCCCATAGCGGGAGGCGCTTGCAGCGCTTTCGCCCACTTCACTGAGCTGG	781
Qy	392	CTATCTCAGCGTCCAACTTATCTGAGTTCGCGAAGGATTCGCGAGGTTGCCAAGA	451
Db	782	CCATCGTCTCTGTCGAGAGATGTTGACTTTGCTTAAACAGCTACCGGCTTCTCGAGC	841
Qy	452	TCTCGAGCTGATCAAAATACGCTGTCTTAAGGCTTGTCTCAAGTGAGTATGATGCTCC	511
Db	842	TCAGCGGGAGGACCAATGTCCTCTGCTGAAGACTCTGCGATCGAGTGTGTTCTGG	901
Qy	512	GAGTTCGCGGACGATACGATGCGGCTCAGACAGTTCCTGTTTCGCGAACAACCAAGCT	571
Db	902	AGACATCTCGGNGTACAACTCGGAGTGAGATATCACCTTCTCTCAAGGATTCAGTT	961
Qy	572	ACACTCGGACAACTACCGGAGGCTGGCATG---GCTAGCTCATCGAGATCTACTGC	628
Db	962	ATAACCGGGAAGACTTTTGCAGGAGGCTGCAAGTGGAAATTCATCAACCCCATCTTCG	1021
Qy	629	ACTTCTCGGCTGATGATCTACTATGCGTTTGGACAAACATCCATTAAGCGCTGCTCAGG	688
Db	1022	AGTTCTCGAGGCGCATGAATGAGCTGCAACTCAATGATGCGAGTTTGCCTTGTCTATTG	1081
Qy	689	CTGTGCTCATCTTTTCT---GACCGGCGAGGTTGGAGCAGCCGCAACTGGTGAAGAAA	745
Db	1082	CTATCAGCATCTTCTCTGACAGCCGCGCCAAACGTCGAGGACAGCTCCAGGTGGAGGC	1141
Qy	746	TCAGCGGTACTACTGAATACGCTCCGCATCTATATCTTGAACAGCAGTGAAGGGTGG	805
Db	1142	TGCAGCACATATGTGGAGCCCTGATGCTTCTAGCTTCTCATCCACC-----ATC	1192
Qy	806	CGCGTTCGTTCGTTCATATACGGCAAGATCTCTCAATCTCTCTGAGTACGACGCTCG	865
Db	1193	CCATGACCGGCTGATGTTCCCAAGATGCTTAATGAACCTGGTGAAGCTTCGAGCCCTGA	1252
Qy	866	GCATGCAAACTCAACATGTGATCTCTCCCTCAAGCTCAAGAACAGAAAGCTGCCGCTT	925
Db	1253	GCAGCGTCCACTCAGAGCAAGTGTTCGACTGCGTCTGCGAGCAAAAGAGCTCCACCGC	1312
Qy	926	TCCTCGAGGAGATCTGGATGTGGCGGA	953
Db	1313	TGCTCTCTGAGATCTGGGATGTGCACGA	1340

RESULT 10
 US-11-166-412-2
 ; Sequence 2, Application US/11166412
 ; Publication No. US20060014231A1

; GENERAL INFORMATION:
 ; APPLICANT: Van Rompaey, Luc
 ; APPLICANT: Tomme, Peter H. M.
 ; TITLE OF INVENTION: Methods and Compositions To Promote Bone Homeostasis
 ; FILE REFERENCE: P27,927-D USA
 ; CURRENT APPLICATION NUMBER: US/11/166,412
 ; CURRENT FILING DATE: 2005-06-24
 ; PRIOR APPLICATION NUMBER: 60/582,704
 ; PRIOR FILING DATE: 2004-06-24
 ; PRIOR APPLICATION NUMBER: 60/630,449
 ; PRIOR FILING DATE: 2004-11-23
 ; PRIOR APPLICATION NUMBER: 60/673,206
 ; PRIOR FILING DATE: 2005-04-20
 ; NUMBER OF SEQ ID NOS: 231
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 2
 ; LENGTH: 1528
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-11-166-412-2

Query Match 9.0%; Score 94.4; DB 8; Length 1528;
 Best Local Similarity 49.3%; Pred. No. 1e-16;
 Matches 369; Conservative 0; Mismatches 361; Indels 18; Gaps 4;

Qy	215	AAAAATCCCCCAGTGTGACAGCCCAACAGAGTTCCTTATCGCCAGGCTCATCTGTATCC	274
Db	637	AAATCTCTGCCCACTGAGCCCGGAACAACTGGGCATGATCGAAGCTCTGCTGCTGCC	696
Qy	275	AGACGGGTACGAGCAGCTTCTGATGAAGATTTGAAGAGATTTACGACAGCTGGCAGC	334
Db	697	AGCAACAGTGAACCGGCGCTTCTTTCTGACCGGCTTTCGAGTCAAGCTTGGCCCATGG	756
Qy	335	AAGCGAGCATGAAGAAACGAAGATC---TGACATCTCCCTTCGCGCAGATCAAGATGA	391
Db	757	CACAGATCTCCCATAGCGGGAGGCGCTGAGAGCGCTTTCGCCATTTCACTGAGCTGG	816
Qy	392	CTATCTCTCAGCGTCCAACTTATCTGAGTTCGCGAAGGATTCGCGAGGTTGCCAAGA	451
Db	817	CCATCGTCTCTGTCGAGGAGATGTTGACTTTGCTTAAACAGCTACCGGCTTCTGCGAGC	876
Qy	452	TCGCGAGCTGATCAAAATTAAGCTGCTTAAGGCTTCTCAAGTGAAGTAAATGATGCTCC	511
Db	877	TCAGCGGAGGAGCAGATGTCCTTCTGTAAGACTCTGCGATCGAGTGTGATGCTCTGG	936
Qy	512	GAGTTCGCGGACGATACGATGCGGCTCAGACAGTGTCTGTTTCGCGAACAACCAAGCT	571
Db	937	AGACATCTCGAGGATCAACCTTGGGAGTGAGAGTATCACTTCTCTCAAGATTTCAAGTT	996
Qy	572	ACACTCGGACAACTACCGCAAGGCTGGCATG---GCTTACGTCATCGAGGATCTACTGC	628
Db	997	ATAACCGGGAAGACTTTGCGCAAGAGGCGCTGCAAGTGGAAATTCATCAACCCCATCTTCG	1056
Qy	629	ACTTCTCGCGGTGATGATCTCTATGCGGTGGAGCAACATCCATTAAGCGCTGCTCAGG	688
Db	1057	AGTTCTCTCAGGGCGGATGATGAGTGCACATCAATGATGCGGATTTGCGCTTGTCTCATTTG	1116
Qy	689	CTGTGCTCATCTTTTCT---GACCGGCGAGGTTGGAGCAGCCGCAACTGCTGGAAGAAA	745
Db	1117	CTATCAGCATCTTCTCTGACAGCCGCGCCAACTGCGAGGAGGCTTCAGGTGGAGGCG	1176
Qy	746	TCAGCGGTACTACTGAATACGCTCCGCATCTATATCTTGAACAGCAGCTGAGCGGTTCGG	805
Db	1177	TGCAGCACATATGTGGAGCCCTGATGCTTCTAGCTTCTCATCCACC-----ATC	1227
Qy	806	CGCGTTCGTTCGTTCATATACGGCAAGATCTCTCAATCTCTCTGAGCTACGACGCTCG	865
Db	1228	CCATGACCGACTGATGTTCCACGCGGATGCTTAATGAACCTGCTGAGGCTTCGAGACCTGA	1287
Qy	866	GCATGCAAACTCAACATGTGATCTCTCCCTCAAGCTCAGAACAGAAAGCTCGGCTT	925
Db	1288	GCAGCGTCCACTCAGAGCAAGTGTTCGACTGCGTCTGCGAGCAAAAGAGCTCCACCGC	1347

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QY 926 TCCTCGAGGAGATCTGGGATGTGGCGGA 953
Db 1348 TGCTCTCGAGATCTGGGATGTGGCAGCA 1375

RESULT 11
US-11-136-527-2936
; Sequence 2936, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2936
; LENGTH: 2156
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-2936

Query Match 7.2%; Score 75.8; DB 8; Length 2156;
Best Local Similarity 49.4%; Pred. No. 2.2e-11;
Matches 222; Conservative 1; Mismatches 223; Indels 3; Gaps 1;

QY 375 CCAGATCACAGAGATGACTATCTCCAGGTCCTCACTGCTGAGTTCCTGCTGAGTTCGCGAGGAGTT 434
Db 909 CAAGTTCAAGTGAATCTCTCCACCAAGTATCATYARGACTGTGGAGTTCCGCCAAGAGCT 968
QY 435 GCCAGGGTTCCGCAAGATCTCGCAGCCTGATCAAAATTACGCTGCTTAAGGCTTGTCTCAAG 494
Db 969 TCCGGGCTTCAACACCTCACCATTGCCAGCAGATTTACCTTTCTCAAGGCTGCCT 1028
QY 495 TGAGTGAATGCTCGAGTTCGGGCGACATAGGATGGCGCTTCAGAGCTTGTCTGTT 554
Db 1029 GGACATCTGATTTCTGGAAATTCGCACGCGGTACACCTTGAGCAAGACACAATGACCTT 1088
QY 555 CGCGAACCAACCAAGCGTACACTCGCGACAACTACCGCAAGGCTGGCATGCGCTACGTCAT 614
Db 1089 CTGATGAGTGAATGCTTCAAGCGGACTGAGATGCAACAGCTGTGCTTGGCCCTTCA 1148
QY 615 CGAGGATCTACTGCACTTCTGCGGTGTCATGTACTCTATGGCGTTGGACAACTCCATTA 674
Db 1149 CGACTTGGTCTTTGGCTTGGCCAAACAGCTGCTGCCCTGGAGATGGACGATGCTGAGAC 1208
QY 675 CGCGTGTCTACGGCTGT----CGTCATCTTTTCGACCGGCCAGGGTTGGAGCGCGCA 731
Db 1209 CGGACTGCTCAGTGCCATCTGCTCCTCATCTGTGGAGACCGACAGGACCTGGAGCGCCAGA 1268
QY 732 ACTGGTGGAAAGAAATCAGCGGTACTACCTGAAATAGCTCGCATCTATATCTCTGAACCA 791
Db 1269 CAAGTGGAATGCTGCGAGGCGCGTGTGGAGCACTGAAGTCTATGTTCGGAACG 1328
QY 792 GCTGAGCGGTTCGGCGGTTGTCGTCGTC 820
Db 1329 GAGGCCAGCRRCCCCACATGTTCCCA 1357

RESULT 12
US-11-136-527-1966
; Sequence 1966, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
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; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1966
; LENGTH: 2329
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-1966

Query Match 7.0%; Score 74; DB 8; Length 2329;
Best Local Similarity 50.5%; Pred. No. 7.4e-11;
Matches 195; Conservative 4; Mismatches 184; Indels 3; Gaps 1;

QY 413 TCGTGAGTTTCGGAAGGATTCGCCAGGTTTCGTCGCAAGATCTCGCAGCCTGATCAAAATTA 472
Db 1532 TGGTAGAATTTGCCAAACAGATCCCGGCTTCCGTGACCTTCTCAGCAGCAGCAGGTGA 1591
QY 473 CGCTGCTTAAGGCTTCTCTCAAGTGAGGTAATGATGCTCCGAGTTCGCGCGCAGATACGATG 532
Db 1592 CCCTGCTTAAGGCTGGCACCCTTTGAGGTGCTGATGGTGGGCTTTGGGTCAATGTTCAACG 1651
QY 533 CGGCCTCAGACAGTGTTCGTTTCGCGAACAACCAAGCGTACACTCGCGCAACTACCGCA 592
Db 1652 TGAGGACACAGACAGTATGTTCTGAGCGCGCAACCTACAGCCTGCAGGAGTCCGGT 1711
QY 593 AGGCTGGCATGGCTACGTCATCGAGGATCTACTGCACCTTCTGCCGGTGCATGTACTCTA 652
Db 1712 CCATGGCATGGTGGACCTGCTCAATGCCATGTTTGACWTGAGGAGAGCTCACTCTIS 1771
QY 653 TGGCGTTGGACAAACATCCATTTAGCGCTGCTCAGCGCTGCTCAGCGCTGCG---TCATCTTTTCTGACC 709
Db 1772 TGGCGTTTACTGAGGAGGAGCTGGGCTTTTTCAGCGCAGTGGTACTTGTCTCTGCAGASS 1831
QY 710 GGCGAGGTTTGGAGCAGCGCAACTGGTGGAGAAATCCAGCGGTACTACCTGAATACGC 769
Db 1832 GCTCGGAAATGAGAAATTCGGTTCGGTGGAGAGCTCAGGAGACGCTGCTGGGGGCTC 1891
QY 770 TCGCATCTATATCTCTGAACCCAGCTG 795
Db 1892 TTCGGGCTCTGCTGCTGAAGACCG 1917

RESULT 13
US-11-112-908-15
; Sequence 15, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 15
; LENGTH: 2355
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-15

Query Match 6.4%; Score 67.6; DB 8; Length 2355;
Best Local Similarity 50.3%; Pred. No. 4.7e-09;
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QY 721 GAGCAGCGCAACTGGTGGAGAAATCCAGCGGTACTACCTGAATAGCTCCGCATCTAT 780
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Db 1135 CAGGACCGAGTCCCAAGTAGRGRGACTGCAACACACATWTGTGGAGGCCCTGCATGCCCKWK 1194
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 781 ATCCTGAACCAAGCTGAGCGGGTCGGCGGTTTCGTCGTCAATATACGCGCAAGATCCTCTCA 840
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1195 GTVTCATCAACCAACCCCAAGACCGAY-----TGATGTTCCACGGATGYTAATG 1245
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 841 ATCCTCTCTGAGCTACGACGCTCGGCATGCAAACTCCAAACATGTGCATCTCCCTCAAG 900
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1246 AAGYTGGTGAAGCTCCGGACTTTGAGCAGCGTCCCATTCAGAGCAAGTGTTCACATTCCG 1305
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 901 CTCAGAACAGAAAGCTGCCGCTTTCTCGAGGAGATCTGGGATGTGGCGGA 953
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1306 CTCAGAGCAAAAAMTTCCCTTGTCTTCCGAGATYGGGATGTCCMCGA 1358
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Search completed: January 31, 2006, 16:57:42
 Job time : 402 secs


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Qy 181 CTCTCCGCAAGCTGTTGGAGACAAACCGGCGAGAAAAATCCCCAGTTGACAGCAAC 240
Db 181 CTCTCCGCAAGCTGTTGGAGACAAACCGGCGAGAAAAATCCCCAGTTGACAGCAAC 240
Qy 241 CAGCAGTTCCTTATCGCCAGGCTCATCTGGTACGAGCAGGTTACGAGCAGCCTTCTGAT 300
Db 241 CAGCAGTTCCTTATCGCCAGGCTCATCTGGTACGAGCAGGTTACGAGCAGCCTTCTGAT 300
Qy 301 GAAGATTGGAAGAGATTACGAGACGTGCGAGCAAGCGGACGATGAAAAAGAGAGTCT 360
Db 301 GAAGATTGGAAGAGATTACGAGACGTGCGAGCAAGCGGACGATGAAAAAGAGAGTCT 360
Qy 361 GACATCCCTTCGCGCAGATCACAGAGATGACTATCTCAGCGTCCAACTTATCGTGAG 420
Db 361 GACATCCCTTCGCGCAGATCACAGAGATGACTATCTCAGCGTCCAACTTATCGTGAG 420
Qy 421 TTCCGGAAGGAGATTGCGCAAGGTTGCGCAAGATCTCGCAGCCTGATCAAAATAGCGTCT 480
Db 421 TTCCGGAAGGAGATTGCGCAAGGTTGCGCAAGATCTCGCAGCCTGATCAAAATAGCGTCT 480
Qy 481 AAGCCTTGCTCAAGTGAAGTAAATGATGCTCGAGTCCGCGACGATACGATGCGGCTCA 540
Db 481 AAGCCTTGCTCAAGTGAAGTAAATGATGCTCGAGTCCGCGACGATACGATGCGGCTCA 540
Qy 541 GACAGTCTCTGTTCCGCGAACCAAGCGTACACTCGCGACAACTACCGCAAGGCTGGC 600
Db 541 GACAGTCTCTGTTCCGCGAACCAAGCGTACACTCGCGACAACTACCGCAAGGCTGGC 600
Qy 601 ATGSCCTACGTCATCGAGGATCTACTGCACTTCTGCGGTTGCACTGATCTATGGCGTTG 660
Db 601 ATGSCCTACGTCATCGAGGATCTACTGCACTTCTGCGGTTGCACTGATCTATGGCGTTG 660
Qy 661 GACAAATCCATTAAGCGTGTGCAAGAAATCAGCGGTACTGTAATAGCTCCGCACTAT 780
Db 661 GACAAATCCATTAAGCGTGTGCAAGAAATCAGCGGTACTGTAATAGCTCCGCACTAT 780
Qy 781 ATCTCGAACCAAGCTGAGCGGTGCGCGCTTCTCGTCCGTATATACGGCAAGATCTCTCA 840
Db 781 ATCTCGAACCAAGCTGAGCGGTGCGCGCTTCTCGTCCGTATATACGGCAAGATCTCTCA 840
Qy 841 ATCTCTCTGAGCTACGCAAGCTCGGATGCAAAATCCCAACATGTCGATCTCCCTCAG 900
Db 841 ATCTCTCTGAGCTACGCAAGCTCGGATGCAAAATCCCAACATGTCGATCTCCCTCAG 900
Qy 901 CTCAAGAACAGAAAGCTGCGCGCTTCTCTGAGGAGATCTGGGATGCGGAGATGTCG 960
Db 901 CTCAAGAACAGAAAGCTGCGCGCTTCTCTGAGGAGATCTGGGATGCGGAGATGTCG 960
Qy 961 CACACCCAAACCGCGCTTATCTCGAGTCCCGCCAGAACTCTAGCCCTCGCGCACGC 1020
Db 961 CACACCCAAACCGCGCTTATCTCGAGTCCCGCCAGAACTCTAGCCCTCGCGCACGC 1020
Qy 1021 ATGCGGATGCGCGTTCGCGCGCTGCTCTGA 1054
Db 1021 ATGCGGATGCGCGTTCGCGCGCTGCTCTGA 1054

RESULT 2
US-10-239-134-3
; Sequence 3, Application US/10239134
; Publication No. US20040033600A1
; GENERAL INFORMATION:
; APPLICANT: Rohm and Haas Company
; APPLICANT: Palli, Subba Reddy
; APPLICANT: Kapitehaya, Marianna Zinovjevna
; APPLICANT: Cress, Dean Ervin
; TITLE OF INVENTION: No. US20040033600A1e1 Ecdysone Receptor-Based Inducible Gene Expr
; FILE REFERENCE: RH0020
; CURRENT APPLICATION NUMBER: US/10/239,134
```

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; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: 60/191,355
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/269,799
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 1054
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: No. US20040033600A1e1 Sequence
US-10-239-134-3

Query Match 100.0%; Score 1054; DB 7; Length 1054;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1054; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTGAGTGGTGTAGTACCCGAGACTCAGTGGCCATGAAGCGGAAAGAGAAAGACAG 60
Db 1 CCTGAGTGGTGTAGTACCCGAGACTCAGTGGCCATGAAGCGGAAAGAGAAAGACAG 60
Qy 61 AAGGAGAGAGACAAACTGCTCTCAGCAGACGACGCGGTGACGACCAATGCCCATTT 120
Db 61 AAGGAGAGAGACAAACTGCTCTCAGCAGACGACGCGGTGACGACCAATGCCCATTT 120
Qy 121 ATGCACTGTGAACCTCCACTCTCTGAAGCAGCAAGGATTCAGCAAGTGGTCCCAAGGTTT 180
Db 121 ATGCACTGTGAACCTCCACTCTCTGAAGCAGCAAGGATTCAGCAAGTGGTCCCAAGGTTT 180
Qy 181 CTCTCCGCAAGCTGTTGGAGACAAACCGCGAGAAAAATATCCCCAGTTGACAGCAAC 240
Db 181 CTCTCCGCAAGCTGTTGGAGACAAACCGCGAGAAAAATATCCCCAGTTGACAGCAAC 240
Qy 241 CAGCAGTCTCTTATCGCCAGGCTCATCTGGTACCAAGGACGCGGTACGAGCAGCCTTCTGAT 300
Db 241 CAGCAGTCTCTTATCGCCAGGCTCATCTGGTACCAAGGACGCGGTACGAGCAGCCTTCTGAT 300
Qy 301 GAAGATTGGAAGAGATTACGAGACGTGCGAGCAAGCGGACGATGAAAAAGAGAGTCT 360
Db 301 GAAGATTGGAAGAGATTACGAGACGTGCGAGCAAGCGGACGATGAAAAAGAGAGTCT 360
Qy 361 GACATCCCTTCGCGCAGATCACAGAGATGACTATCTCCTCAAGCTTATCGTGAG 420
Db 361 GACATCCCTTCGCGCAGATCACAGAGATGACTATCTCCTCAAGCTTATCGTGAG 420
Qy 421 TTCCGGAAGGAGATTGCGCAAGGTTGCGCAAGATCTCGCAGCCTGATCAAAATAGCGTCT 480
Db 421 TTCCGGAAGGAGATTGCGCAAGGTTGCGCAAGATCTCGCAGCCTGATCAAAATAGCGTCT 480
Qy 481 AAGCCTTGCTCAAGTGAAGTAAATGATGCTCGAGTCCGCGACGATACGATGCGGCTCA 540
Db 481 AAGCCTTGCTCAAGTGAAGTAAATGATGCTCGAGTCCGCGACGATACGATGCGGCTCA 540
Qy 541 GACAGTGTCTTGTTCGCGAACCAAGCGTACACTCGCGACAACTACCGCAAGGCTGGC 600
Db 541 GACAGTGTCTTGTTCGCGAACCAAGCGTACACTCGCGACAACTACCGCAAGGCTGGC 600
Qy 601 ATGCGCTTACGTCATCGAGGATCTACTGCACTTCTGCGGTTGCACTGATCTATGGCGTTG 660
Db 601 ATGCGCTTACGTCATCGAGGATCTACTGCACTTCTGCGGTTGCACTGATCTATGGCGTTG 660
Qy 661 GACAAATCCATTAAGCGTGTGCAAGAAATCAGCGGTACTGTAATAGCTCCGCACTAT 720
Db 661 GACAAATCCATTAAGCGTGTGCAAGAAATCAGCGGTACTGTAATAGCTCCGCACTAT 720
Qy 721 GAGCAGCGCAACTGTTGGAGACAAATCAGCGGTACTGTAATAGCTCCGCACTAT 780
Db 721 GAGCAGCGCAACTGTTGGAGACAAATCAGCGGTACTGTAATAGCTCCGCACTAT 780
Qy 781 ATCTGAAACCAAGCTGAGCGGTGCGCGCTTCTCGTCCGTATATACGGCAAGATCTCTCA 840
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Db 781 ATCTGAAACAGCTGAGCGGTGCGCGTTCGTCGATATACGGCAAGATCTCTCA 840
Qy 841 ATCTCTCTGAGCTACGACGCTCGGATGCAAACTCTCAACATGTGCATCTCTCAAG 900
Db 841 ATCTCTCTGAGCTACGACGCTCGGATGCAAACTCTCAACATGTGCATCTCTCAAG 900
Qy 901 CTCAAGAACAGAAAGCTGCGCTCTCTCTGAGAGATCTGGATGTGGCGGACATGTGCG 960
Db 901 CTCAAGAACAGAAAGCTGCGCTCTCTCTGAGAGATCTGGATGTGGCGGACATGTGCG 960
Qy 961 CACACCAACCGCGCTATCTCTGAGTCCGCCACGATCTCTAGCCCTCGCGGACGC 1020
Db 961 CACACCAACCGCGCTATCTCTGAGTCCGCCACGATCTCTAGCCCTCGCGGACGC 1020
Qy 1021 ATCCCGATGCGCGTCCGCGCGCTCTCTGA 1054
Db 1021 ATCCCGATGCGCGTCCGCGCGCTCTCTGA 1054

RESULT 3

US-10-468-199-65
; Sequence 65, Application US/10468199
; Publication No. US20040096942A1
; GENERAL INFORMATION:
; APPLICANT: Palli, Subba R.
; APPLICANT: Kapitekaya, Marianna Z.
; TITLE OF INVENTION: Chimeric retinoid X receptors and their use in a novel ecdysone
; TITLE OF INVENTION: Receptor-based inducible gene expression system
; FILE REFERENCE: A01238-US
; CURRENT APPLICATION NUMBER: US/10/468,199
; CURRENT FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/294,819
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: PCT/US02/05706
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 65
; LENGTH: 1054
; TYPE: DNA
; ORGANISM: Choristoneura fumiferana
US-10-468-199-65

Query Match 100.0%; Score 1054; DB 7; Length 1054;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1054; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTGAGTGGCTAGTACCGGACTCAGTGGCGCCATGAAGCGGAAGAGAAAGCAAG 60
Db 1 CCTGAGTGGCTAGTACCGGACTCAGTGGCGCCATGAAGCGGAAGAGAAAGCAAG 60
Qy 61 AAGGAGAGGACAACTGCTGTGAGCAGCAGCGTGGAGCAGCAGTCCGCCCATTT 120
Db 61 AAGGAGAGGACAACTGCTGTGAGCAGCAGCGTGGAGCAGCAGTCCGCCCATTT 120
Qy 121 ATGCAAGTGTGAACCTCCACCTCTCTGAAGCAAGGATTTACAGAGTGGTCCCAAGGTTT 180
Db 121 ATGCAAGTGTGAACCTCCACCTCTCTGAAGCAAGGATTTACAGAGTGGTCCCAAGGTTT 180
Qy 181 CTCTCCGACAGCTGTTGGAGACAAACCGGAGAAAAACATCCGCCAGTTGACAGCCAAAC 240
Db 181 CTCTCCGACAGCTGTTGGAGACAAACCGGAGAAAAACATCCGCCAGTTGACAGCCAAAC 240
Qy 241 CAGCAGTCTTATGCGCAGGCTATCTGGTACAGGACGGGTACGAGCAGCCTTCTGAT 300
Db 241 CAGCAGTCTTATGCGCAGGCTATCTGGTACAGGACGGGTACGAGCAGCCTTCTGAT 300
Qy 301 GAAGATTTGAAGAGATTTACGACAGCTGGCAGCAGCGAGATGAAGAAAGAGAGTCT 360
Db 301 GAAGATTTGAAGAGATTTACGACAGCTGGCAGCAGCGAGATGAAGAAAGAGAGTCT 360
Qy 361 GACATCCCTTCCGCCAGATCACAGAGATGATCTCTCACGGTCCAACTTATCGTGGAG 420

Db 361 GACATCCCTTCCGCCAGATCACAGAGATGATCTCTCACGGTCCAACTTATCGTGGAG 420
Qy 421 TTCCGGAAGGATTTCCAGGGTTCGCAAGATCTCGAGCTGATCAAAATTTACGCTGCTT 480
Db 421 TTCCGGAAGGATTTCCAGGGTTCGCAAGATCTCGAGCTGATCAAAATTTACGCTGCTT 480
Qy 481 AAGGCTTGTCTCAAGTGAAGTAATGATCTCGAGTTCGCGGACGATACGATGCGGCTCA 540
Db 481 AAGGCTTGTCTCAAGTGAAGTAATGATCTCGAGTTCGCGGACGATACGATGCGGCTCA 540
Qy 541 GACAGTGTCTGTTCCGGAACCAAGCGGTACACTCGGACCAACTACCGCAAGGCTGGC 600
Db 541 GACAGTGTCTGTTCCGGAACCAAGCGGTACACTCGGACCAACTACCGCAAGGCTGGC 600
Qy 601 ATGGCCTTACGTTCATCGAGGATCTACTGCACCTTTCGCGGTGTCATGTACTTATGGCGTTG 660
Db 601 ATGGCCTTACGTTCATCGAGGATCTACTGCACCTTTCGCGGTGTCATGTACTTATGGCGTTG 660
Qy 661 GACAAATCCATTAACGCGTCTCACGCGTGTCTCATCTTTTCTGACCGGCCAGGGTTG 720
Db 661 GACAAATCCATTAACGCGTCTCACGCGTGTCTCATCTTTTCTGACCGGCCAGGGTTG 720
Qy 721 GAGCAGCGCACTGTGTGGAGAAATCCAGCGGTACTACCTGAATACGCTCCGATCTAT 780
Db 721 GAGCAGCGCACTGTGTGGAGAAATCCAGCGGTACTACCTGAATACGCTCCGATCTAT 780
Qy 781 ATCTCTGAACAGCTGAGCGGTGCGCGTTCGTCGCTCATATACGGCAAGATCTCTCA 840
Db 781 ATCTCTGAACAGCTGAGCGGTGCGCGTTCGTCGCTCATATACGGCAAGATCTCTCA 840
Qy 841 ATCTCTCTGAGCTACGACGCTCGGATGCAAAACTCCCAACATGTGCATCTCCCTCAAG 900
Db 841 ATCTCTCTGAGCTACGACGCTCGGATGCAAAACTCCCAACATGTGCATCTCCCTCAAG 900
Qy 901 CTCAAGAACAGAAAGCTGCGCGCTTTCCTCGAGAGATCTGGAGTGTGGCGGACATGTGCG 960
Db 901 CTCAAGAACAGAAAGCTGCGCGCTTTCCTCGAGAGATCTGGAGTGTGGCGGACATGTGCG 960
Qy 961 CACACCAACCGCGCTATCTCTGAGTCCGCCACGATCTCTAGCCCTCGCGGACGC 1020
Db 961 CACACCAACCGCGCTATCTCTGAGTCCGCCACGATCTCTAGCCCTCGCGGACGC 1020
Qy 1021 ATCCCGATGCGCGTCCGCGCGCTCTCTGA 1054
Db 1021 ATCCCGATGCGCGTCCGCGCGCTCTCTGA 1054

RESULT 4

US-10-783-810-1
; Sequence 1, Application US/10783810
; Publication No. US20040171651A1
; GENERAL INFORMATION:
; APPLICANT: Hormann, Robert E
; APPLICANT: Chortyk, Orestes
; APPLICANT: Le, Dat Phat
; TITLE OF INVENTION: Oxadiazoline ligands for modulating the expression of exogenous
; FILE REFERENCE: A01494-US
; CURRENT APPLICATION NUMBER: US/10/783,810
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US 60/449,467
; PRIOR FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1054
; TYPE: DNA
; ORGANISM: Choristoneura fumiferana
US-10-783-810-1

Query Match 100.0%; Score 1054; DB 7; Length 1054;
Best Local Similarity 100.0%; Pred. No. 0;

		Matches 1054; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	CTGTAGTGGTGTAGTACCGAGACTCAGTGGCCCATGAGCGGAAAGAGAAAGACACAG	60		
Db	1	CTGTAGTGGTGTAGTACCGAGACTCAGTGGCCCATGAGCGGAAAGAGAAAGACACAG	60		
Qy	61	AAGGAGAGGACAAATCGCTGTGACGACGACGAGGTGACGACACATGCGGCCATT	120		
Db	61	AAGGAGAGGACAAATCGCTGTGACGACGACGAGGTGACGACACATGCGGCCATT	120		
Qy	121	ATGCAAGTGAACCTCCACTCTGAGGACGAGGATTCAGGAAGTGTGCCAAGGTTT	180		
Db	121	ATGCAAGTGAACCTCCACTCTGAGGACGAGGATTCAGGAAGTGTGCCAAGGTTT	180		
Qy	181	CTCTCCGACAAAGCTGTGGAGACAAACCGGACAGAAATCATCCGCCATTGACAGCCAAC	240		
Db	181	CTCTCCGACAAAGCTGTGGAGACAAACCGGACAGAAATCATCCGCCATTGACAGCCAAC	240		
Qy	241	CAGCAGTTCCTTATCGCCAGGCTCATCTGGTACGAGCGGTACGAGCGCTTCTGAT	300		
Db	241	CAGCAGTTCCTTATCGCCAGGCTCATCTGGTACGAGCGGTACGAGCGCTTCTGAT	300		
Qy	301	GAAGATTTGAAGAGGATTAACGACAGCTGCGACGACGATGAATAACGAAGAGTCT	360		
Db	301	GAAGATTTGAAGAGGATTAACGACAGCTGCGACGACGATGAATAACGAAGAGTCT	360		
Qy	361	GACACTCCCTTCGCCAGATCAAGAGATGACTATCTCAGCGTCCAACTTATCGTGGAG	420		
Db	361	GACACTCCCTTCGCCAGATCAAGAGATGACTATCTCAGCGTCCAACTTATCGTGGAG	420		
Qy	421	TTCCGCAAGGATTTGCCAGGTTTGCACAGATCTCGCAGCTCATCAAAATACGCTGCTT	480		
Db	421	TTCCGCAAGGATTTGCCAGGTTTGCACAGATCTCGCAGCTCATCAAAATACGCTGCTT	480		
Qy	481	AAGGCTTGCTCAAGTGAAGGATTAACGACAGCTGCGACGACGATGAATAACGAAGAGTCT	540		
Db	481	AAGGCTTGCTCAAGTGAAGGATTAACGACAGCTGCGACGACGATGAATAACGAAGAGTCT	540		
Qy	541	GACAGTGTCTGTTCGGGAAACAAAGCGTACACTCGCGACAACTACCGCAAGGCTGGC	600		
Db	541	GACAGTGTCTGTTCGGGAAACAAAGCGTACACTCGCGACAACTACCGCAAGGCTGGC	600		
Qy	601	ATGCGCTTACGTCTAGGAGTACTGCACTTCTCGCGGTGATGATCTATGCGGTG	660		
Db	601	ATGCGCTTACGTCTAGGAGTACTGCACTTCTCGCGGTGATGATCTATGCGGTG	660		
Qy	661	GACAACTATCAACGCTGCTCAGCGCTGTGCTCATCTTTTCTGACCGGCCAGGGTTG	720		
Db	661	GACAACTATCAACGCTGCTCAGCGCTGTGCTCATCTTTTCTGACCGGCCAGGGTTG	720		
Qy	721	GAGCAGCGCAACTGTGTGGAAGAAATCCAGCGGTATACCTGAAATACGCTCCGATCTAT	780		
Db	721	GAGCAGCGCAACTGTGTGGAAGAAATCCAGCGGTATACCTGAAATACGCTCCGATCTAT	780		
Qy	781	ATCTGAAACAGCTGAGCGGTGGCGGTGCTGCTGCTATATATGCGCAAGATCTCTCA	840		
Db	781	ATCTGAAACAGCTGAGCGGTGGCGGTGCTGCTGCTATATATGCGCAAGATCTCTCA	840		
Qy	841	ATCTCTCTGAGCTACGACGCTGGGATGCAAACTCCAACTATGTCATCTCCCTCAAG	900		
Db	841	ATCTCTCTGAGCTACGACGCTGGGATGCAAACTCCAACTATGTCATCTCCCTCAAG	900		
Qy	901	CTCAGAAACAGAGTGGCGCTTCTCTGAGGAGATCTGGGATGTGGGAGCATGTGCG	960		
Db	901	CTCAGAAACAGAGTGGCGCTTCTCTGAGGAGATCTGGGATGTGGGAGCATGTGCG	960		
Qy	961	CACACCAACCGCGCTATCTCGAGTCCCGCAAGTCTCTAGCCCTTCGCGGACGCG	1020		
Db	961	CACACCAACCGCGCTATCTCGAGTCCCGCAAGTCTCTAGCCCTTCGCGGACGCG	1020		
Qy	1021	ATCGCGATGCGCGTCCGCGCGCTGCTCTGA	1054		
Db	1021	ATCGCGATGCGCGTCCGCGCGCTGCTCTGA	1054		

RESULT 5
 US-10-775-883-1
 ; Sequence 1, Application US/10775883
 ; Publication No. US20050209283A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hormann, Robert E
 ; APPLICANT: Chortyk, Orestes
 ; APPLICANT: Smith, Howard
 ; APPLICANT: Meteyer, Thomas
 ; APPLICANT: Tice, Colin M
 ; TITLE OF INVENTION: DIACYLHYDRAZINE LIGANDS FOR MODULATING THE EXPRESSION OF
 ; FILE REFERENCE: A01381-US
 ; CURRENT FILING DATE: 2004-02-09
 ; PRIOR FILING DATE: 2003-02-10
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 1
 ; LENGTH: 1054
 ; TYPE: DNA
 ; ORGANISM: Choriostoneura fumiferana
 US-10-775-883-1

		Query Match 100.0%; Score 1054; DB 9; Length 1054; Best Local Similarity 100.0%; Pred. No. 0; Matches 1054; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	CTGTAGTGGTGTAGTACCGAGACTCAGTGGCCCATGAGCGGAAAGAGAAAGACACAG	60		
Db	1	CTGTAGTGGTGTAGTACCGAGACTCAGTGGCCCATGAGCGGAAAGAGAAAGACACAG	60		
Qy	61	AAGGAGAGGACAAATCGCTGTGACGACGACGAGGTGACGACACATGCGGCCATT	120		
Db	61	AAGGAGAGGACAAATCGCTGTGACGACGACGAGGTGACGACACATGCGGCCATT	120		
Qy	121	ATGCAAGTGAACCTCCACTCTGAGGACGAGGATTCAGGAAGTGTGCCAAGGTTT	180		
Db	121	ATGCAAGTGAACCTCCACTCTGAGGACGAGGATTCAGGAAGTGTGCCAAGGTTT	180		
Qy	181	CTCTCCGACAAAGCTGTGGAGACAAACCGGACAGAAATCATCCGCCATTGACAGCCAAC	240		
Db	181	CTCTCCGACAAAGCTGTGGAGACAAACCGGACAGAAATCATCCGCCATTGACAGCCAAC	240		
Qy	241	CAGCAGTTCCTTATCGCCAGGCTCATCTGGTACCGAGCGGTACGAGCGCTTCTGAT	300		
Db	241	CAGCAGTTCCTTATCGCCAGGCTCATCTGGTACCGAGCGGTACGAGCGCTTCTGAT	300		
Qy	301	GAAGATTTGAAGAGGATTAACGACAGCTGCGACGACGATGAATAACGAAGAGTCT	360		
Db	301	GAAGATTTGAAGAGGATTAACGACAGCTGCGACGACGATGAATAACGAAGAGTCT	360		
Qy	361	GACACTCCCTTCGCCAGATCAAGAGATGACTATCTCAGCGTCCAACTTATCGTGGAG	420		
Db	361	GACACTCCCTTCGCCAGATCAAGAGATGACTATCTCAGCGTCCAACTTATCGTGGAG	420		
Qy	421	TTCCGCAAGGATTTGCCAGGTTTGCACAGATCTCGCAGCTCATCAAAATACGCTGCTT	480		
Db	421	TTCCGCAAGGATTTGCCAGGTTTGCACAGATCTCGCAGCTCATCAAAATACGCTGCTT	480		
Qy	481	AAGGCTTGCTCAAGTGAAGGATTAACGACAGCTGCGACGACGATGAATAACGAAGAGTCT	540		
Db	481	AAGGCTTGCTCAAGTGAAGGATTAACGACAGCTGCGACGACGATGAATAACGAAGAGTCT	540		
Qy	541	GACAGTGTCTGTTCGGGAAACAAAGCGTACACTCGCGACAACTACCGCAAGGCTGGC	600		
Db	541	GACAGTGTCTGTTCGGGAAACAAAGCGTACACTCGCGACAACTACCGCAAGGCTGGC	600		
Qy	601	ATGCGCTTACGTCTAGGAGTACTGCACTTCTCGCGGTGATGATCTATGCGGTG	660		

[illegible]

RESULT 6

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US-09-965-703-1
; Sequence 1, Application US/09965703
; Patent No. US20020119521A1
; GENERAL INFORMATION:
; APPLICANT: Rohm and Haas Company
; APPLICANT: Palli, Subba Reddy
; APPLICANT: Kapitskaya, Marianna Zinovjevna
; APPLICANT: Cress, Dean Ervin
; TITLE OF INVENTION: No. US20020119521A1el Ecdysone Receptor-Based Inducible Gene Expr
; FILE REFERENCE: A01020B
; CURRENT APPLICATION NUMBER: US/09/965,703
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/191,355
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/269,799
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: PCT/US01/09050
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1288
; TYPE: DNA
; ORGANISM: Choriostoneura fumiferana
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: No. US20020119521A1el Sequence
US-09-965-703-1

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Query Match	100.0%	Score 1054	DB 3	Length 1288
Best Local Similarity	100.0%	Pred. NO. 0		
Matches 1054	Conservative 0	Mismatches 0	Indels 0	Gaps 0

1	CTTGAGTGGCGTAGTATCCCGAGATCTCAGTGGCCCATGAAGCGGAAAGAGAGAAAGCACAG	60
Qy		
235	CTTGAGTGGCGTAGTATCCCGAGATCTCAGTGGCCCATGAAGCGGAAAGAGAGAAAGCACAG	294
Db		
61	AAGGAGAAGGACAAACTGCTGTGTGACGACGACGCGGTGGACGACACATGCCGCCCATTT	120
Qy		
295	AAGGAGAAGGACAAACTGCTGTGTGACGACGACGCGGTGGACGACACATGCCGCCCATTT	354
Db		

; APPLICANT: Kapitskaya, Marianna Zinovjevna
 ; APPLICANT: Cress, Dean Ervin
 ; TITLE OF INVENTION: No. US20040033600A1e1 Rodyone Receptor-Based Inducible Gene Expression
 ; FILE REFERENCE: RH0020
 ; CURRENT FILING DATE: 2002-09-19
 ; PRIOR FILING DATE: 2002-03-22
 ; PRIOR FILING DATE: 2000-03-22
 ; PRIOR APPLICATION NUMBER: 60/269,799
 ; PRIOR FILING DATE: 2001-02-20
 ; NUMBER OF SEQ ID NOS: 64
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 1288
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: No. US20040033600A1e1 Sequence
 ; US-10-239-134-1

Query Match 100.0%; Score 1054; DB 7; Length 1288;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1054; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	CTGTAGTGGTGTAGTACCCGAGACTCAGTGGCCATGAGCGGAAAGAGAAAGACACAG	60
Db	235	CTGTAGTGGTGTAGTACCCGAGACTCAGTGGCCATGAGCGGAAAGAGAAAGACACAG	294
Qy	61	AAGGAGAGACAACTGCTGTCAGCAGCAGCGGTGACGACCAATGCGCCCATTT	120
Db	295	AAGGAGAGACAACTGCTGTCAGCAGCAGCGGTGACGACCAATGCGCCCATTT	354
Qy	121	ATGCAGTGTAACTCCACCTCTGAGCAGCAGGATTCAGCAAGTGTGCTCCAAAGGTTT	180
Db	355	ATGCAGTGTAACTCCACCTCTGAGCAGCAGGATTCAGCAAGTGTGCTCCAAAGGTTT	414
Qy	181	CTCTCCGAGCAAGCTGTGGAGCAAAACCGCGCAGAAAACATCCCCAGTTGACAGCAAC	240
Db	415	CTCTCCGAGCAAGCTGTGGAGCAAAACCGCGCAGAAAACATCCCCAGTTGACAGCAAC	474
Qy	241	CAGCAGTTCCTTATCGCAGGCTCATCTGTTACGAGCGGTACGAGCAGCTTCTGAT	300
Db	475	CAGCAGTTCCTTATCGCAGGCTCATCTGTTACGAGCGGTACGAGCAGCTTCTGAT	534
Qy	301	GAAGATTTGAAGAGATTACGACAGCTGGCAGCAAGCGGACGATGAAAACGAAGAGTCT	360
Db	535	GAAGATTTGAAGAGATTACGACAGCTGGCAGCAAGCGGACGATGAAAACGAAGAGTCT	594
Qy	361	GACACTCCCTTCGCGCAGATCAGAGATGACTATCTCAGCGTCCAACTTATCGTGGAG	420
Db	595	GACACTCCCTTCGCGCAGATCAGAGATGACTATCTCAGCGTCCAACTTATCGTGGAG	654
Qy	421	TTCCGAGAGGATTTGCCAGGTTTCCGCAAGATCTCGCAGGCTGATCAAAATTCAGCTGCTT	480
Db	655	TTCCGAGAGGATTTGCCAGGTTTCCGCAAGATCTCGCAGGCTGATCAAAATTCAGCTGCTT	714
Qy	481	AAGCTTTGCTCAAGTGAAGTAAATGATCTCCGAGTCCGCGGACGATACGATGCGGCTCA	540
Db	715	AAGCTTTGCTCAAGTGAAGTAAATGATCTCCGAGTCCGCGGACGATACGATGCGGCTCA	774
Qy	541	GACAGTGTCTGTTCGCGAACAACCAAGCGGTACACTCGCGAACAATACCGCAAGGCTGGC	600
Db	775	GACAGTGTCTGTTCGCGAACAACCAAGCGGTACACTCGCGAACAATACCGCAAGGCTGGC	834
Qy	601	ATGCGCTACCTTCAGAGGATCTACTGCACTTCGCGGTCGATGTACTCTATGGCGTTG	660
Db	835	ATGCGCTACCTTCAGAGGATCTACTGCACTTCGCGGTCGATGTACTCTATGGCGTTG	894
Qy	661	GACAACTTCAATACGCGCTGCTCAGCGGCTGTGTCTATCTTTTCTGACCGCGCAGGCTTG	720
Db	895	GACAACTTCAATACGCGCTGCTCAGCGGCTGTGTCTATCTTTTCTGACCGCGCAGGCTTG	954

Qy	721	GAGCAGCCCAACTGTTGGAAGAAATCCAGCGGTACTACTGAATACGCTCCGCACTTAT	780
Db	955	GAGCAGCCCAACTGTTGGAAGAAATCCAGCGGTACTACTGAATACGCTCCGCACTTAT	1014
Qy	781	ATCTCTGAACACAGCTGAGCGGTCGGCGGCTTCTCGTTCATATACGCGCAAGATCTCTCA	840
Db	1015	ATCTCTGAACACAGCTGAGCGGTCGGCGGCTTCTCGTTCATATACGCGCAAGATCTCTCA	1074
Qy	841	ATCTCTCTGAGCTACGACAGCTCGGCATGCAAAACTCCAAATGTCATCTCCCTCAAG	900
Db	1075	ATCTCTCTGAGCTACGACAGCTCGGCATGCAAAACTCCAAATGTCATCTCCCTCAAG	1134
Qy	901	CTCAAGAACAGAAAGCTGCGGCTTCTCTGAGGAGATCTGGGATGCGGCAATGTCG	960
Db	1135	CTCAAGAACAGAAAGCTGCGGCTTCTCTGAGGAGATCTGGGATGCGGCAATGTCG	1194
Qy	961	CACACCAACCGCGGCTTCTCTGAGTCCCGCAGAACTCTTAGCCCTGCGCGCAGCG	1020
Db	1195	CACACCAACCGCGGCTTCTCTGAGTCCCGCAGAACTCTTAGCCCTGCGCGCAGCG	1254
Qy	1021	ATGCGCGATGCGCGGTCGCGCGCGCTGCTCTGA	1054
Db	1255	ATGCGCGATGCGCGGTCGCGCGCGCTGCTCTGA	1288

RESULT 8
 US-10-468-199-59
 ; Sequence 59, Application US/10468199
 ; Publication No. US20040096942A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Palli, Subba R.
 ; APPLICANT: Kapitskaya, Marianna Z.
 ; TITLE OF INVENTION: Chimeric retinoid X receptors and their use in a novel ecdysone
 ; FILE REFERENCE: receptor-based inducible gene expression system
 ; CURRENT APPLICATION NUMBER: US/10/468,199
 ; PRIOR FILING DATE: 2002-02-20
 ; PRIOR APPLICATION NUMBER: US 60/294,819
 ; PRIOR FILING DATE: 2001-05-31
 ; PRIOR APPLICATION NUMBER: PCT/US02/05706
 ; PRIOR FILING DATE: 2002-02-20
 ; NUMBER OF SEQ ID NOS: 75
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 59
 ; LENGTH: 1288
 ; TYPE: DNA
 ; ORGANISM: Choristoneura fumiferana
 ; US-10-468-199-59

Query Match 100.0%; Score 1054; DB 7; Length 1288;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1054; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	CTGTAGTGGTGTAGTACCCGAGACTCAGTGGCCATGAGCGGAAAGAGAAAGACACAG	60
Db	235	CTGTAGTGGTGTAGTACCCGAGACTCAGTGGCCATGAGCGGAAAGAGAAAGACACAG	294
Qy	61	AAGGAGAGACAACTGCTGTCAGCAGCAGCGGTGACGACCAATGCGCCCATTT	120
Db	295	AAGGAGAGACAACTGCTGTCAGCAGCAGCGGTGACGACCAATGCGCCCATTT	354
Qy	121	ATGCAGTGTAACTCCACCTCTGAGCAGCAGGATTCAGCAAGTGTGCTCCAAAGGTTT	180
Db	355	ATGCAGTGTAACTCCACCTCTGAGCAGCAGGATTCAGCAAGTGTGCTCCAAAGGTTT	414
Qy	181	CTCTCCGAGCAAGCTGTGGAGCAAAACCGCGCAGAAAACATCCCCAGTTGACAGCAAC	240
Db	415	CTCTCCGAGCAAGCTGTGGAGCAAAACCGCGCAGAAAACATCCCCAGTTGACAGCAAC	474
Qy	241	CAGCAGTTCCTTATCGCAGGCTCATCTGTTACGAGCGGTACGAGCAGCTTCTGAT	300
Db	475	CAGCAGTTCCTTATCGCAGGCTCATCTGTTACGAGCGGTACGAGCAGCTTCTGAT	534


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Qy 301 GAAGATTGAAGAGGATTACACAGACGTGGCAGCAAGCGGACGATGAAAAAGAGAGTCT 360
Db 535 GAAGATTGAAGAGGATTACACAGACGTGGCAGCAAGCGGACGATGAAAAAGAGAGTCT 594
Qy 361 GACACTCCCTCCGCGAGATCAGAGAGTACTATCTCAGGTCCTCAACTTATCGTGGAG 420
Db 595 GACACTCCCTCCGCGAGATCAGAGAGTACTATCTCAGGTCCTCAACTTATCGTGGAG 654
Qy 421 TTCGCGAAGGATTGCGCAGGTTCCGCAAGATCTCGCAGCCTGATCAAAATACGCTGCTT 480
Db 655 TTCGCGAAGGATTGCGCAGGTTCCGCAAGATCTCGCAGCCTGATCAAAATACGCTGCTT 714
Qy 481 AAGGCTTGCTCAAGTGAAGTAAATGATGCTCCGAGTCGCGAGCGATACGATCGGCTTCA 540
Db 715 AAGGCTTGCTCAAGTGAAGTAAATGATGCTCCGAGTCGCGAGCGATACGATCGGCTTCA 774
Qy 541 GACAGTGTCTGTTCCGGAACCAACGAGTACACTCGCGACACTACGCAAGGCTGGC 600
Db 775 GACAGTGTCTGTTCCGGAACCAACGAGTACACTCGCGACACTACGCAAGGCTGGC 834
Qy 601 ATGGCTTACGTCATCGAGGATCTACTGCACTTCTGCGCGGTGATGTAATCTATGGCGTTG 660
Db 835 ATGGCTTACGTCATCGAGGATCTACTGCACTTCTGCGCGGTGATGTAATCTATGGCGTTG 894
Qy 661 GACAAATCCATTACGGCTGCTCAAGGCTGTCTGATCTCTTTCTGACCGGCTCAGGTTG 720
Db 895 GACAAATCCATTACGGCTGCTCAAGGCTGTCTGATCTCTTTCTGACCGGCTCAGGTTG 954
Qy 721 GAGCAGCGGCACTGTTGGAGAAATCCAGCGGTACTACCTGAATACGCTCCGATCTAT 780
Db 955 GAGCAGCGGCACTGTTGGAGAAATCCAGCGGTACTACCTGAATACGCTCCGATCTAT 1014
Qy 781 ATCTGTAACAGCTGAGCGGTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
Db 1015 ATCTGTAACAGCTGAGCGGTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1074
Qy 841 ATCTCTCTGAGTACGCAAGCTCGGATCGCAATGCAAACTCCAACTGTCATCTCCCTCAAG 900
Db 1075 ATCTCTCTGAGTACGCAAGCTCGGATCGCAATGCAAACTCCAACTGTCATCTCCCTCAAG 1134
Qy 901 CTGAAGACAGAAAGCTGCGGCTTCTCTGAGGAGATCTGGGATGTTGGGACATGTCG 960
Db 1135 CTGAAGACAGAAAGCTGCGGCTTCTCTGAGGAGATCTGGGATGTTGGGACATGTCG 1194
Qy 961 CACACCAACCGCGCTTATCTCTGAGTCCCGCAGCAATCTAGCCCTCGCGCGCAGC 1020
Db 1195 CACACCAACCGCGCTTATCTCTGAGTCCCGCAGCAATCTAGCCCTCGCGCGCAGC 1254
Qy 1021 ATGCGGATGCGGCTCGGCGGCTGCTCTGA 1054
Db 1255 ATGCGGATGCGGCTCGGCGGCTGCTCTGA 1288
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RESULT 9
US-09-965-697-4
; Sequence 4, Application US/09965697
; Patent No. US20020110861A1
; GENERAL INFORMATION:
; APPLICANT: Hormann, Robert E.
; APPLICANT: Palli, Subba Reddy
; APPLICANT: Carlson, Glenn R.
; APPLICANT: Cress, Dean E.
; APPLICANT: Dhadialla, Tarlochan S.
; APPLICANT: Herzig, Ronald P.
; APPLICANT: Kudia, Arthur J.
; APPLICANT: Philip, Mohan
; TITLE OF INVENTION: Multiple Inducible Gene Regulation System
; FILE REFERENCE: RH-0036 (DN A01115A)
; CURRENT APPLICATION NUMBER: US/09/965,697
; PRIORITY FILING DATE: 2001-09-27
; PRIORITY FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 16

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; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 1290  
; TYPE: DNA  
; ORGANISM: Choristoneura fumiferana  
US-09-965-697-4  
  
Query Match 97.7%; Score 1029.4; DB 3; Length 1290;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 1052; Conservative 0; Mismatches 1; Indels 2; Gaps 2;  
  
Qy 1 CCTGAGTGCCTAGTACCCGAGACTCAGTGGCCCATGGAAGCGGAAAGAGAAAGCAAGCAG 60  
Db 237 CCTGAGTGCCTAGTACCCGAGACTCAGTGGCCCATGGAAGCGGAAAGAGAAAGCAAGCAG 296  
Qy 61 AAGGAGAAAGCAAACTGCTGTGACGACGACGCTGACGACCAATGCGCCCATTT 120  
Db 297 AAGGAGAAAGCAAACTGCTGTGACGACGACGCTGACGACCAATGCGCCCATTT 356  
Qy 121 ATGCAAGTGTGAACCTCCACCTCTGGAAGCAGCAAGGATTCACGAAAGTGGTCCCAAGGTTT 180  
Db 357 ATGCAAGTGTGAACCTCCACCTCTGGAAGCAGCAAGGATTCACGAAAGTGGTCCCAAGGTTT 416  
Qy 181 CTCTCCGACAAAGCTGTTGGAGACAAACCGCGGAGAAACATCCCCGACGTTGACAGCCAAC 240  
Db 417 CTCTCCGACAAAGCTGTTGGAGACAAACCGCGGAGAAACATCCCCGACGTTGACAGCCAAC 476  
Qy 241 CAGCAGTTCCTTATTCGCGCAGGCTCATCTGTGTACGAGACGGGTACGAGCAGCCTTCTGAT 300  
Db 477 CAGCAGTTCCTTATTCGCGCAGGCTCATCTGTGTACGAGACGGGTACGAGCAGCCTTCTGAT 536  
Qy 301 GAAGATTGAAGAGGATTACGAGACGCTGGCAGCAAGCGGACGATGAAAAAGAGAGTCT 360  
Db 537 GAAGATTGAAGAGGATTACGAGACGCTGGCAGCAAGCGGACGATGAAAAAGAGAGTCT 596  
Qy 361 GACACTCCCTTCGCGCAGATCAGAGATGATCTATCTCAGGTCCTCAACTTATCGTGGAG 420  
Db 597 GACACTCCCTTCGCGCAGATCAGAGATGATCTATCTCAGGTCCTCAACTTATCGTGGAG 656  
Qy 421 TTGCGGAAGGAGTTCGCGAGGTTGCGCAAGATCTCGCAGCCTGATCAAAATACGCTGCTT 480  
Db 657 TTGCGGAAGGAGTTCGCGAGGTTGCGCAAGATCTCGCAGCCTGATCAAAATACGCTGCTT 716  
Qy 481 AAGGCTTGCTCAAGTGAAGTAAATGATGCTCCGAGTCGCGGACGATACGATCGGCGCTCA 540  
Db 717 AAGGCTTGCTCAAGTGAAGTAAATGATGCTCCGAGTCGCGGACGATACGATCGGCGCTCA 776  
Qy 541 GACAGTGTCTGTTGCGGAAACAAACGAGCTGTAATCTCGGACCAACTACGCGCAAGGCTGGC 600  
Db 777 GACAGTGTCTGTTGCGGAAACAAACGAGCTGTAATCTCGGACCAACTACGCGCAAGGCTGGC 836  
Qy 601 ATGGCCTACGTCATCGAGGATCTACTGCACTTCTGCGGCTGCAATGTAATCTATGGCGTTG 660  
Db 837 ATGGCCTACGTCATCGAGGATCTACTGCACTTCTGCGGCTGCAATGTAATCTATGGCGTTG 896  
Qy 661 GACAAATCCATTACGCGCTGCTCAGCGCTGTCTGATCTTTTCTGACCGGCTCAGGTTG 720  
Db 897 GACAAATCCATTACGCGCTGCTCAGCGCTGTCTGATCTTTTCTGACCGGCTCAGGTTG 956  
Qy 721 GAGCAGCGCAACTGTTGGAGAAATCCAGCGGTACTACCTGAATACGCTCCGATCTAT 780  
Db 957 GAGCAGCGCAACTGTTGGAGAAATCCAGCGGTACTACCTGAATACGCTCCGATCTAT 1016  
Qy 781 ATCTGTAACAGCTGAGCGGTTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840  
Db 1017 ATCTGTAACAGCTGAGCGGTTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1076  
Qy 841 ATCTCTCTGAGTACGCAAGCTCGGATGCAAACTCCCAACATGTCATCTCCCTCAAG 900  
Db 1077 ATCTCTCTGAGTACGCAAGCTCGGATGCAAACTCCCAACATGTCATCTCCCTCAAG 1136  
Qy 901 CTGAAGAAAGCAAGCTGCGGCTTCTCTGAGGAGATCTGGGATGTTGGC-GGACATGTC 959  
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Db 1137 CTCAAGAACAAAGAGTGCAGGCTTTCTCGAGAGATCGGATGTGGCAGGACATGTC 1196
Qy 960 GCACACCCACCGCGCTATCTCGAGTCCCGCCACGAAATCTTAGCCCTCGCGCAG 1019
Db 1197 GCACACCCACCGCGCGCTAT-CTCGAGTCCCGCCACGAAATCTTAGCCCTCGCGCAG 1255
Qy 1020 CATCGCGGATCGCGGCTCGCGCGCGCTGCTCTGA 1054
Db 1256 CATCGCGGATCGCGGCTCGCGCGCGCTGCTCTGA 1290

RESULT 10

US-09-965-697-14

; Sequence 14, Application US/09965697

; Patent No. US20020110861A1

; GENERAL INFORMATION:

; APPLICANT: Hormann, Robert E.

; APPLICANT: Palli, Subba Reddy

; APPLICANT: Carlson, Glenn R.

; APPLICANT: Crees, Dean E.

; APPLICANT: Dhadiella, Tarlochan S.

; APPLICANT: Herzog, Ronald P.

; APPLICANT: Rudla, Arthur J.

; APPLICANT: Philip, Mohan

; TITLE OF INVENTION: Multiple Inducible Gene Regulation System

; FILE REFERENCE: RH-0036 (DN A01115A)

; CURRENT APPLICATION NUMBER: US/09/965,697

; CURRENT FILING DATE: 2001-09-27

; PRIOR FILING DATE: 2000-10-03

; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 14

; LENGTH: 1073

; TYPE: DNA

; ORGANISM: Choristoneura fumiferana

US-09-965-697-14

Query Match 95.8%; Score 1010.2; DB 3; Length 1073;

Best Local Similarity 99.2%; Pred. No. 0;

Matches 1047; Conservative 0; Mismatches 3; Indels 5; Gaps 3;

Qy 1 CCTGAGTGCCTAGTACCGGAGACTCAGTGCCTATGAAGCGGAAAGAGAAAGACACAG 60
Db 1 CCTGAGTGCCTAGTACCGGAGACTCAGTGCCTATGAAGCGGAAAGAGAAAGACACAG 60
Qy 61 AAGGAGAGACAAATGCTCTGTGACGACGAGCGGTGGACGACCAATGCCGCCCAT 120
Db 61 AAGGAGAGACAAATGCTCTGTGACGACGAGCGGTGGACGACCAATGCCGCCCAT 120
Qy 121 ATGAGTGTGAACCTTCCACTCTGAAAGCAGCAAGGATTACGAGTGGTCCGAGGTTT 180
Db 121 ATGAGTGTGAACCTTCCACTCTGAAAGCAGCAAGGATTACGAGTGGTTCGAGGTTT 180
Qy 181 CTCTCCGACAGCTGTTGGAGACAAACCGGACGAAACATCCCGAGTTGACAGCCAAC 240
Db 181 CTCTCCGACAGCTGTTGGAGACAAACCGGACGAAACATCCCGAGTTGACAGCCAAC 240
Qy 241 CAGCAGTTCCTTATGCGCAGGCTCATCTGGTACGAGACGGGTACGAGCGCTTCTGAT 300
Db 241 CAGCAGTTCCTTATGCGCAGGCTCATCTGGTACGAGACGGGTACGAGCGCTTCTGAT 300
Qy 301 GAAGATTTGAAGAGATTACGACAGCTGCGACGACGAGCGAGTGAAGAGAGTCT 360
Db 301 GAAGATTTGAAGAGATTACGACAGCTGCGACGAGCGAGTGAAGAGAGTCT 360
Qy 361 GACACTCCCTCCCGCAGATCAGAGATGACTATCTCAGGTCGCTTATCGTGGAG 420
Db 361 GACACTCCCTCCCGCAGATCAGAGATGACTATCTCAGGTCGCTTATCGTGGAG 420
Qy 421 TTCCGAGAGGATTTGCCAGGTTCCGCAAGATTCGCGAGCTGATCAAAATTAAGCTGCTT 480
Db 421 TTCCGAGAGGATTTGCCAGGTTCCGCAAGATTCGCGAGCTGATCAAAATTAAGCTGCTT 480

Qy 481 AAGGCTTGTCTCAAGTGAAGTATGATGCTCGAGTCCGCGGAGCATACGATGGGCTCA 540
Db 481 AAGGCTTGTCTCAAGTGAAGTATGATGCTCGAGTCCGCGGAGCATACGATGGGCTCA 537
Qy 541 GACAGTGTCTGTTCCGGAACAAACAAAGCGTACACTCGCGCAAACTACCGCAAGGCTGGC 600
Db 538 GACAGTGTCTGTTCCGGAACAAACAAAGCGTACACTCGCGCAAACTACCGCAAGGCTGGC 597
Qy 601 ATGGCCTACGTCATCGAGGATCTACTGCACTTTCTGCGGTGCAATGCTCTATGGCGTTG 660
Db 598 ATGGCCTACGTCATCGAGGATCTACTGCACTTTCTGCGGTGCAATGCTCTATGGCGTTG 657
Qy 661 GACACATCCATTCAGCGCTGCTCAGCGGTGCTGTCATCTTTTCTGACCGCGCAGGTTG 720
Db 658 GACACATCCATTCAGCGCTGCTCAGCGGTGCTGTCATCTTTTCTGACCGCGCAGGTTG 717
Qy 721 GAGCAGCGCAACTGCTGGAAGAAATCCAGCGGTACTACTGATATAGCTCCGATCTAT 780
Db 718 GAGCAGCGCAACTGCTGGAAGAAATCCAGCGGTACTACTGATATAGCTCCGATCTAT 777
Qy 781 ATCTGAACCAAGTGAAGCGGTGCGCGCTTCTGCTCATATACGCGCAAGATCTCTCA 840
Db 778 ATCTGAACCAAGTGAAGCGGTGCGCGCTTCTGCTCATATACGCGCAAGATCTCTCA 837
Qy 841 ATCTCTCTGAGTACGCGCTGCGCGCTTCTGCTCATATACGCGCAAGATCTCTCA 900
Db 838 ATCTCTCTGAGTACGCGCTGCGCGCTTCTGCTCATATACGCGCAAGATCTCTCA 897
Qy 901 CTCAAGAACAGAAAGTGCAGCGCTTCTGCGAGGAGATCTGGGATGTCGCG-AGACATGTC 959
Db 898 CTCAAGAACAGAAAGTGCAGCGCTTCTGCGAGGAGATCTGGGATGTCGCGAGCATGTC 957
Qy 960 GCACACCCAAACCGCGCTTATCTCGAGTCCCGCCAGAAATCTTAGCCCTCGCGCAG 1019
Db 958 GCACACCCAAACCGCGCTTAT-CTCGAGTCCCGCCAGAAATCTTAGCCCTCGCGCAG 1016
Qy 1020 CATCGCGGATCGCGCTGCGCGCGCTGCTCTGA 1054
Db 1017 CATCGCGGATCGCGCTGCGCGCGCTGCTCTGA 1051

RESULT 11

US-10-614-116-1

; Sequence 1, Application US/10614116

; Publication No. US20040049037A1

; GENERAL INFORMATION:

; APPLICANT: Tice, Colin M

; APPLICANT: Michelotti, Enrique L

; APPLICANT: Hormann, Robert E

; TITLE OF INVENTION: Ketones for modulating the expression of exogenous genes via an

; FILE REFERENCE: A01386us

; CURRENT APPLICATION NUMBER: US/10/614,116

; CURRENT FILING DATE: 2003-07-03

; PRIOR APPLICATION NUMBER: 60/393,960

; PRIOR FILING DATE: 2002-07-05

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 1

; LENGTH: 1073

; TYPE: DNA

; ORGANISM: Choristoneura fumiferana

US-10-614-116-1

Query Match 95.8%; Score 1010.2; DB 7; Length 1073;

Best Local Similarity 99.2%; Pred. No. 0;

Matches 1047; Conservative 0; Mismatches 3; Indels 5; Gaps 3;

Qy 1 CCTGAGTGCCTAGTACCGGAGACTCAGTGCCTATGAAGCGGAAAGAGAAAGACACAG 60
Db 1 CCTGAGTGCCTAGTACCGGAGACTCAGTGCCTATGAAGCGGAAAGAGAAAGACACAG 60

Qy	61	AAGAGAGAGGCAAACTCGCTGTGACGACGACGACGAGCGGTGGACGACCAATCGCGCCCATTT	120
Db	61	AAGAGAGAGGCAAACTCGCTGTGACGACGACGACGAGCGGTGGACGACCAATCGCGCCCATTT	120
Qy	121	ATGCAGTGTGAACCTCCACCTCTCTGAAGCAGCAAGGATTACGAAAGTGGTCCCAAGGTTT	180
Db	121	ATGCAGTGTGAACCTCCACCTCTCTGAAGCAGCAAGGATTACGAAAGTGGTTCGAAGGTTT	180
Qy	181	CTCTCCGACAAGCTGTTGGAGACAAAACCGGCAGAAAAAATCCTCCCGAGTTGACAGCCAAAC	240
Db	181	CTCTCCGACAAGCTGTTGGAGACAAAACCGGCAGAAAAAATCCTCCCGAGTTGACAGCCAAAC	240
Qy	241	CAGCAGTTCTTATTCGCCAGGCTCATCTGTGTACAGGACGGGTACGAGCAGCCTTCTGTAT	300
Db	241	CAGCAGTTCTTATTCGCCAGGCTCATCTGTGTACAGGACGGGTACGAGCAGCCTTCTGTAT	300
Qy	301	GAAGATTTGAAGAGGATTTACGCAGACGTGGCAGCAAGCGGACGATGAAAAAGAGAGTCT	360
Db	301	GAAGATTTGAAGAGGATTTACGCAGACGTGGCAGCAAGCGGACGATGAAAAAGAGAGTCT	360
Qy	361	GACACTGCTTTCGCCAGATCACAGAGATGACTATCTCTCAGCGTCCAACTTATCGTGAG	420
Db	361	GACACTGCTTTCGCCAGATCACAGAGATGACTATCTCTCAGCGTCCAACTTATCGTGAG	420
Qy	421	TTCCGAAAGGATTTGCCAGGGTTCGCCAAGATCTCGCAGCCTGATCAAAATTCAGCTCGTT	480
Db	421	TTCCGAAAGGATTTGCCAGGGTTCGCCAAGATCTCGCAGCCTGATCAAAATTCAGCTCGTT	480
Qy	481	AAGGCTTTGCTCAAGTGAGTAAATGATGCTCCGAGTTCGCGACGATACGATCGCGCCTCA	540
Db	481	AAGGCTTTGCTCAAGTGAGTAAATGATGCTCCGAGTTCGCGACGATACGATCGCGCCTCA	537
Qy	541	GACAGTGTCTGTTGCGGACAAACCAAGCGTACACTCGCGACAACTACCGCAAGGCTGBC	600
Db	538	GACAGTGTCTGTTGCGGACAAACCAAGCGTACACTCGCGACAACTACCGCAAGGCTGBC	597
Qy	601	ATGCGCTTACGTATCGAGGATCTACTGCACTTCTGCGCGTGATGTACTCTATGCGGTG	660
Db	598	ATGCGCTTACGTATCGAGGATCTACTGCACTTCTGCGCGTGATGTACTCTATGCGGTG	657
Qy	661	GACAACTCCAATTACGCGCTGCTCACGCGTGTGCTCATCTTTCTGACCGGCCAGGGTTG	720
Db	658	GACAACTCCAATTACGCGCTGCTCACGCGTGTGCTCATCTTTCTGACCGGCCAGGGTTG	717
Qy	721	GAGCAGCGGCAACTGGTGGAGAAATCCAGCGGTACTACCTGATATACGCTCGCATCTAT	780
Db	718	GAGCAGCGGCAACTGGTGGAGAAATCCAGCGGTACTACCTGATATACGCTCGCATCTAT	777
Qy	781	ATCTCTGAACAGCTGAGCGGTCGGCGTTCGCTCATATACGCAAGATCCTCTCA	840
Db	778	ATCTCTGAACAGCTGAGCGGTCGGCGTTCGCTCATATACGCAAGATCCTCTCA	837
Qy	841	ATCTCTCTGAGCTACGACGCTCGGATGCAAAACTCCAAATATGTGCATCTCCCTCAAG	900
Db	838	ATCTCTCTGAGCTACGACGCTCGGATGCAAAACTCCAAATATGTGCATCTCCCTCAAG	897
Qy	901	CTCAAGAACAGAGCTGCGGCTTTCTCTGAGAGATCTGGGATGTGGC--GGAATGTC	959
Db	898	CTCAAGAACAGAGCTGCGGCTTTCTCTGAGAGATCTGGGATGTGGC--GGAATGTC	957
Qy	960	GCAACCCAAACCGCGCTTATCTCTGAGTCCCGCAAGAACTCTTAGGCCCTCGCGGACG	1019
Db	958	GCAACCCAAACCGCGCTTAT--CTCGAGTCCCGCAAGAACTCTTAGGCCCTCGCGGACG	1016
Qy	1020	CATCGCGATGCGCGTTCGCGCGCGCTGCTCTGA	1054
Db	1017	CATCGCGATGCGCGTTCGCGCGCGCTGCTCTGA	1051

RESULT 12

US-10-460-820-1

US-10-460-820-1
; Sequence 1, Application US/10460820

; sequence 1, Application US/1048
; Publication No. US20050228016A1

QY 721 GAGCAGCGCAACTGGTGGAGAAATCCAGCGGTACTACTGAATACGCTCCGCACTAT 780
DB 718 GAGCAGCGCAACTGGTGGAGAAATCCAGCGGTACTACTGAATACGCTCCGCACTAT 777
QY 781 ATCTGAACAGCTGAGCGGGTCCGCGGTTGCTCGGTATATACGCGCAAGATCTCTCTCA 840
DB 778 ATCTGAACAGCTGAGCGGGTCCGCGGTTGCTCGGTATATACGCGCAAGATCTCTCTCA 837
QY 841 ATCTCTCTGAGTACGCAAGCTCGGATGCAAAATCTCCAGATGCGATCTCCCTCAAG 900
DB 838 ATCTCTCTGAGTACGCAAGCTCGGATGCAAAATCTCCAGATGCGATCTCCCTCAAG 897
QY 901 CTCAAGAACAGAAAGCTGCGCGCTTTCTCGAGAGATCTGGATGTGGC-GGACATGTC 959
DB 898 CTCAAGAACAGAAAGCTGCGCGCTTTCTCGAGAGATCTGGATGTGGCAGCAATGTC 957
QY 960 GCACACCAACCGCGCTATCTCGAGTCCCGCAAGATCTCTAGCCCTCGCGCAGC 1019
DB 958 GCACACCAACCGCGCTAT-CTCGAGTCCCGCAAGATCTCTAGCCCTCGCGCAGC 1016
QY 1020 CATCGCGGATGCGCGTCCGCGCGCGCTGCTCTGA 1054
DB 1017 CATCGCGGATGCGCGTCCGCGCGCGCTGCTCTGA 1051

RESULT 13

US-09-965-703-2
; Sequence 2, Application US/09965703
; Patent No. US20020119521A1
; GENERAL INFORMATION:
; APPLICANT: Rohm and Haas Company
; APPLICANT: Palli, Subba Reddy
; APPLICANT: Kapitskaya, Marianna Zinovjevna
; APPLICANT: Cress, Dean Ervin
; TITLE OF INVENTION: No. US20020119521A1e1 Bcdysone Receptor-Based Inducible Gene Expr
; FILE REFERENCE: A01020B
; CURRENT APPLICATION NUMBER: US/09/965,703
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/191,355
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/269,799
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: PCT/US01/09050
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1110
; TYPE: DNA
; ORGANISM: Choristoneura fumiferana
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: No. US20020119521A1e1 Sequence
US-09-965-703-2

Query Match 95.4%; Score 1005; DB 3; Length 1110;
Best Local Similarity 100.0%; Pred. No. 8.1e-314;
Matches 1005; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCTGAGTGGCTAGTACCCGAGACTCAGTGGCCATGAAGCGGAAAGAGAAAGAACACAG 60
DB 106 CCTGAGTGGCTAGTACCCGAGACTCAGTGGCCATGAAGCGGAAAGAGAAAGAACACAG 165
QY 61 AAGAGAAAGCAAACTGCTGTGACGACGCGGTGGACGACCAATGCGCGCCCAAT 120
DB 166 AAGAGAAAGCAAACTGCTGTGACGACGCGGTGGACGACCAATGCGCGCCCAAT 225
QY 121 ATGCAAGTGAACCTCACTCTGAGAGCAAGGATTCAGCAAGTGGTCCCAAGTTT 180
DB 226 ATGCAAGTGAACCTCACTCTGAGAGCAAGGATTCAGCAAGTGGTCCCAAGTTT 285
QY 181 CTCTCCCAACAGCTGTGGAGACAAACCGGCGAGAAATATCCCGCAAGTTTGACAGCCAAC 240

DB 286 CTCTCCGCAACAGCTGTGGAGACAAACCGCGAGAAABACATCCCCAGTTTGACAGCCAAC 345
QY 241 CAGCAGTTCTTATCGCAGAGCTCATCTGTGTACAGGACGGGTACGAGAGGCTTCTGAT 300
DB 346 CAGCAGTTCTTATCGCAGAGCTCATCTGTGTACAGGACGGGTACGAGAGGCTTCTGAT 405
QY 301 GAAGATTTGAAGAGATTTACGACAGCTGGCAGCAGCGGAGCGGAGATGAAACCAAGATCT 360
DB 406 GAAGATTTGAAGAGATTTACGACAGCTGGCAGCAGCGGAGCGGAGATGAAACCAAGATCT 465
QY 361 GACACTCCCTTCGCGCAGATCAAGAGATGACTATCTCCTCAGCGTCCAACTTATCGTGGAG 420
DB 466 GACACTCCCTTCGCGCAGATCAAGAGATGACTATCTCCTCAGCGTCCAACTTATCGTGGAG 525
QY 421 TTGCGGAAGGATTTGCGCAGGTTTCCCAAGATCTCTCGAGCTTGATCAAAATTAAGCTGCTT 480
DB 526 TTGCGGAAGGATTTGCGCAGGTTTCCCAAGATCTCTCGAGCTTGATCAAAATTAAGCTGCTT 585
QY 481 AAGGCTTGTCTCAAGTGAGTAAATGATCTCCAGTGGCGGACGATACGATCGGCTCTCA 540
DB 586 AAGGCTTGTCTCAAGTGAGTAAATGATCTCCAGTGGCGGACGATACGATCGGCTCTCA 645
QY 541 GACAGTGTCTCTTCGCGAAACCAAGCGTACACTTCGCGACAACTACCGCAAGGCTGCG 600
DB 646 GACAGTGTCTCTTCGCGAAACCAAGCGTACACTTCGCGACAACTACCGCAAGGCTGCG 705
QY 601 ATGGCTTCTCATCGAGATCTTACCTGCACTTTCTCGCGGTGATGTACTCTATAGGCTTG 660
DB 706 ATGGCTTCTCATCGAGATCTTACCTGCACTTTCTCGCGGTGATGTACTCTATAGGCTTG 765
QY 661 GACACATCCATTACGCGTCTCAAGCTGCTGCTCATCTTTCTGACCGGCGCAGGTTG 720
DB 766 GACACATCCATTACGCGTCTGCTCAAGCTGCTGCTCATCTTTCTGACCGGCGCAGGTTG 825
QY 721 GAGCAGCCCAACTGTGTGAAGAAATCCAGCGGTACTACTGAATACGCTCCGCACTAT 780
DB 826 GAGCAGCCCAACTGTGTGAAGAAATCCAGCGGTACTACTGAATACGCTCCGCACTAT 885
QY 781 ATCTGAACAGCTGAGCGGGTCCGCGGTTCTCGGTATATACGCGCAAGATCTCTCTCA 840
DB 886 ATCTGAACAGCTGAGCGGGTCCGCGGTTCTCGGTATATACGCGCAAGATCTCTCTCA 945
QY 841 ATCTCTCTGAGTACGCAAGCTCCGCAATGCAAAATCCAAATGTCATCTCCCTCAAG 900
DB 946 ATCTCTCTGAGTACGCAAGCTCCGCAATGCAAAATCCAAATGTCATCTCCCTCAAG 1005
QY 901 CTCAAGACAGAAAGCTGCGCGCTTTCTCTCGAGGAGATCTGGGATGTGGGACATGTGCG 960
DB 1006 CTCAAGACAGAAAGCTGCGCGCTTTCTCTCGAGGAGATCTGGGATGTGGGACATGTGCG 1065
QY 961 CACACCCAAACCGCGCTTATCTCGAGTCCCGCAAGATCTCTAG 1005
DB 1066 CACACCCAAACCGCGCTTATCTCTCGAGTCCCGCAAGATCTCTAG 1110

RESULT 14

US-10-239-134-2
; Sequence 2, Application US/10239134
; Publication No. US20040033600A1
; GENERAL INFORMATION:
; APPLICANT: Rohm and Haas Company
; APPLICANT: Palli, Subba Reddy
; APPLICANT: Kapitskaya, Marianna Zinovjevna
; APPLICANT: Cress, Dean Ervin
; TITLE OF INVENTION: No. US20040033600A1e1 Bcdysone Receptor-Based Inducible Gene Expr
; FILE REFERENCE: RH0020
; CURRENT APPLICATION NUMBER: US/10/239,134
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: 60/191,355
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/269,799
; PRIOR FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 64

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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 1110
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: No. US20040033600A1el Sequence
US-10-239-134-2

Query Match          95.4%; Score 1005; DB 7; Length 1110;
Best Local Similarity 100.0%; Pred. No. 8.1e-314;
Matches 1005; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTGAGTGGCTAGTACCGGAGACTCAGTGCCTCCATGAAAGCGGAAAGAAAGCAAG 60
Db 106 CCTGAGTGGCTAGTACCGGAGACTCAGTGCCTCCATGAAAGCGGAAAGAAAGCAAG 165
Qy 61 AAGGAGAGGACAAACTGCCTGTGAGCAGCAGGAGGTTGAGCAGCAGCAGCAGCAG 120
Db 166 AAGGAGAGGACAAACTGCCTGTGAGCAGCAGGAGGTTGAGCAGCAGCAGCAGCAG 225
Qy 121 ATGCAGTGTGAACCTCCACCTCTGAGCAGCAGGAGTTTACGAAAGTGGTCCCAAGGTTT 180
Db 226 ATGCAGTGTGAACCTCCACCTCTGAGCAGCAGGAGTTTACGAAAGTGGTCCCAAGGTTT 285
Qy 181 CTCTCCGACAGCTGTTGGAGACAAACCGGAGGAAACATCCCGGAGTTGACAGCCAAAC 240
Db 286 CTCTCCGACAGCTGTTGGAGACAAACCGGAGGAAACATCCCGGAGTTGACAGCCAAAC 345
Qy 241 CAGCAGTTCCTTATCGCAGGCTCATCTGTGACAGCAGGAGTACGAGCAGCCTTCTGAT 300
Db 346 CAGCAGTTCCTTATCGCAGGCTCATCTGTGACAGCAGGAGTACGAGCAGCCTTCTGAT 405
Qy 301 GAAGATTGAGAGGATTAACGACAGCTGAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 360
Db 406 GAAGATTGAGAGGATTAACGACAGCTGAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 465
Qy 361 GACATCCCTTCCTCCAGATCAGAGATGACTATCTCTCAGGTCCTCACTTATCGTGGAG 420
Db 466 GACATCCCTTCCTCCAGATCAGAGATGACTATCTCTCAGGTCCTCACTTATCGTGGAG 525
Qy 421 TTCCGGAAGGATTCGAGGTTCCGCAAGATCTCGCAGCCTGATCAAAATACGCTGCTT 480
Db 526 TTCCGGAAGGATTCGAGGTTCCGCAAGATCTCGCAGCCTGATCAAAATACGCTGCTT 585
Qy 481 AAGGCTTGCTCAAGTGAAGTAAATGATGCTCGAGTCCGCGAGCAGCAGTACGATGCGGCTCA 540
Db 586 AAGGCTTGCTCAAGTGAAGTAAATGATGCTCGAGTCCGCGAGCAGCAGTACGATGCGGCTCA 645
Qy 541 GACAGTGTTCCTGTCGCGAAACAAACGAGCTACACTCGCAGCAACTACCGCAAGGCTGGC 600
Db 646 GACAGTGTTCCTGTCGCGAAACAAACGAGCTACACTCGCAGCAACTACCGCAAGGCTGGC 705
Qy 601 ATGCGCTTCACTGAGGATCTACTGACCTTTCGCGGTGTCATGTAATCTATGCGGTTG 660
Db 706 ATGCGCTTCACTGAGGATCTACTGACCTTTCGCGGTGTCATGTAATCTATGCGGTTG 765
Qy 661 GACAACTCAATTAAGCGGCTGCTCAGCGCTGCTGATCTTCTTTCGCGGAGGTTG 720
Db 766 GACAACTCAATTAAGCGGCTGCTCAGCGCTGCTGATCTTCTTTCGCGGAGGTTG 825
Qy 721 GAGCAGCGGCAACTGAGGAGAAATCCAGCGGTACTACCTGAAATACGCTCCGATCTAT 780
Db 826 GAGCAGCGGCAACTGAGGAGAAATCCAGCGGTACTACCTGAAATACGCTCCGATCTAT 885
Qy 781 ATCTGAAACCAAGCTGAGCGGTTCGCGGTTTCGTCCTCATATATACGCGCAAGATCTCTCA 840
Db 886 ATCTGAAACCAAGCTGAGCGGTTCGCGGTTTCGTCCTCATATATACGCGCAAGATCTCTCA 945
Qy 841 ATCTCTCTGAGCTACGAGCTCGGAGTGCAGAAATCTCCAAACATGTGATCTCCCTCAAG 900
Db 946 ATCTCTCTGAGCTACGAGCTCGGAGTGCAGAAATCTCCAAACATGTGATCTCCCTCAAG 1005
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Qy 901 CTCAGAAACAGAAAGCTGCGCCTTTCTCTCGAGAGATCTGGGATGTGGCGGACATGTCG 960
Db 1006 CTCAGAAACAGAAAGCTGCGCCTTTCTCTCGAGAGATCTGGGATGTGGCGGACATGTCG 1065
Qy 961 CACACCAACCGCGCTATCTCGAGTCCCGCCACGATCTCTAG 1005
Db 1066 CACACCAACCGCGCTATCTCGAGTCCCGCCACGATCTCTAG 1110
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RESULT 15

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US-09-965-703-58
; Sequence 58, Application US/09965703
; Patent No. US20020119521A1
; GENERAL INFORMATION:
; APPLICANT: Rohm and Haas Company
; APPLICANT: Palli, Subba Reddy
; APPLICANT: Kapitekaya, Marianna Zinovjevna
; APPLICANT: Cress, Dean Ervin
; TITLE OF INVENTION: No. US20020119521A1el Bcdysone Receptor-Based Inducible Gene Expr
; FILE REFERENCE: A01020B
; CURRENT APPLICATION NUMBER: US/09/965,703
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/191,355
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/269,799
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: PCT/US01/09050
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58
; LENGTH: 1542
; TYPE: DNA
; ORGANISM: Choristoneura fumiferana
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: No. US20020119521A1el Sequence
US-09-965-703-58
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Query Match          95.4%; Score 1005; DB 3; Length 1542;
Best Local Similarity 100.0%; Pred. No. 8.1e-314;
Matches 1005; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 CCTGAGTGGCTAGTACCGGAGACTCAGTGCCTCCATGAAAGCGGAAAGAAAGCAAG 60
Db 538 CCTGAGTGGCTAGTACCGGAGACTCAGTGCCTCCATGAAAGCGGAAAGAAAGCAAG 597
Qy 61 AAGGAGAGGACAAACTGCCTGTGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 120
Db 598 AAGGAGAGGACAAACTGCCTGTGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 657
Qy 121 ATGCAGTGTGAACCTCCACCTCTGAGCAGCAGGAGTTTACGAAAGTGGTCCCAAGGTTT 180
Db 658 ATGCAGTGTGAACCTCCACCTCTGAGCAGCAGGAGTTTACGAAAGTGGTCCCAAGGTTT 717
Qy 181 CTCTCCGACAGCTGTTGGAGACAAACCGGAGGAAACATCCCGGAGTTGACAGCCAAAC 240
Db 718 CTCTCCGACAGCTGTTGGAGACAAACCGGAGGAAACATCCCGGAGTTGACAGCCAAAC 777
Qy 241 CAGCAGTTCCTTATCGCAGGCTCATCTGGTACAGGAGCGGTTACGAGCAGCCTTCTGAT 300
Db 778 CAGCAGTTCCTTATCGCAGGCTCATCTGGTACAGGAGCGGTTACGAGCAGCCTTCTGAT 837
Qy 301 GAAGATTGAGAGGATTAACGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 360
Db 838 GAAGATTGAGAGGATTAACGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 897
Qy 361 GACATCCCTTCCTCCAGATCAGAGATGACTATCTCTCAGCTCCCAACTTATCTGAGG 420
Db 898 GACATCCCTTCCTCCAGATCAGAGATGACTATCTCTCAGCTCCCAACTTATCTGAGG 957
Qy 421 TTCCGGAAGGATTCGAGGTTCCGCAAGATCTCGCAGCCTCACTTATCGCTGCTT 480
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Db	958	TTCCGAAGGATTGCGAGGTTTCGCCAAGATCTCGCAGCCTCATCAATTAACGTGCTT	1017
Qy	481	AAGGCTTGCTCAAGTAGTAAATGATGCTCCGAGTGGCGGACGATACGATGGGCTCA	540
Db	1018	AAGGCTTGCTCAAGTAGTAAATGATGCTCCGAGTGGCGGACGATACGATGGGCTCA	1077
Qy	541	GACAGTGTCTGTTTCGGCAACCAAGCGTACATCGCGACAACTACCGCAAGGCTGGC	600
Db	1078	GACAGTGTCTGTTTCGGCAACCAAGCGTACATCGCGACAACTACCGCAAGGCTGGC	1137
Qy	601	ATGGCCTACGTACATCGAGGATCTACTGCACTTCTGCGGTGCATGTACTCTATGGGTTG	660
Db	1138	ATGGCCTACGTACATCGAGGATCTACTGCACTTCTGCGGTGCATGTACTCTATGGGTTG	1197
Qy	661	GACAAATCCATTACGGCTGCTCAAGGCTGTGTCATCTTTTCTGACCGGCGAGGTTG	720
Db	1198	GACAAATCCATTACGGCTGCTCAAGGCTGTGTCATCTTTTCTGACCGGCGAGGTTG	1257
Qy	721	GAGCAGCGCAACTGGTGGAGAAATCCAGGGGTACTACCTGAATACGCTCCGCATCTAT	780
Db	1258	GAGCAGCGCAACTGGTGGAGAAATCCAGGGGTACTACCTGAATACGCTCCGCATCTAT	1317
Qy	781	ATCCTGAACCAAGTGAAGGCTGGCGGTTTCGTCCGTATATACGGCAAGATCCTCTCA	840
Db	1318	ATCCTGAACCAAGTGAAGGCTGGCGGTTTCGTCCGTATATACGGCAAGATCCTCTCA	1377
Qy	841	ATCCTCTCTGAGCTACGCAAGCTGGGATGCAAAATCCCAACATGTGCACTCTCCCTCAAG	900
Db	1378	ATCCTCTCTGAGCTACGCAAGCTGGGATGCAAAATCCCAACATGTGCACTCTCCCTCAAG	1437
Qy	901	CTCAAGAACAGAAAGCTGCGGCTTTCTCGAGGAGATCTGGGATGTGGCGGACATGTGG	960
Db	1438	CTCAAGAACAGAAAGCTGCGGCTTTCTCGAGGAGATCTGGGATGTGGCGGACATGTGG	1497
Qy	961	CACACCCAAACCGCGCTATCTCTGAGTCCGCCCAACGAATCTCTAG	1005
Db	1498	CACACCCAAACCGCGCTATCTCTGAGTCCGCCCAACGAATCTCTAG	1542

Search completed: January 31, 2006, 16:50:51
 Job time : 898 secs

Result No.	Score	Query Match	Length	DB	ID	Description	
1	636.4	60.4	2126	3	US-09-393-839-1	Sequence 1, Appli	
2	623.4	59.1	2840	3	US-10-087-167-1	Sequence 1, Appli	
3	621.6	59.0	1500	3	US-10-087-167-67	Sequence 67, Appl	
4	621.6	59.0	1767	3	US-10-087-167-120	Sequence 120, App	
5	617.4	58.6	1863	3	US-10-087-167-136	Sequence 136, App	
6	617.2	58.6	1848	3	US-10-087-167-134	Sequence 134, App	
7	617	58.5	1518	3	US-10-087-167-93	Sequence 93, Appl	
8	617	58.5	3972	3	US-10-087-167-104	Sequence 104, App	
9	616.4	58.5	1428	3	US-10-087-167-128	Sequence 128, App	
10	616.4	58.5	1809	3	US-10-087-167-142	Sequence 142, App	
11	614.2	58.3	1515	3	US-10-087-167-75	Sequence 75, Appl	
12	614.2	58.3	1782	3	US-10-087-167-124	Sequence 124, App	
13	611.4	58.0	1509	3	US-10-087-167-65	Sequence 65, Appl	
14	611.4	58.0	1776	3	US-10-087-167-118	Sequence 118, App	
15	609.6	57.8	1533	3	US-10-087-167-79	Sequence 79, Appl	
16	609.6	57.8	1800	3	US-10-087-167-126	Sequence 126, App	
17	605.6	57.5	1500	3	US-10-087-167-69	Sequence 69, Appl	
18	605.6	57.5	1767	3	US-10-087-167-122	Sequence 122, App	
19	604	57.3	1524	3	US-10-087-167-77	Sequence 77, Appl	
20	603.2	57.2	1800	3	US-10-087-167-147	Sequence 147, App	
21	595.8	55.6	1934	3	US-08-653-648A-2	Sequence 2, Appli	
22	595.8	55.6	1934	3	US-09-564-418-2	Sequence 2, Appli	
23	595.8	55.6	1934	3	US-09-564-418-61	Sequence 61, Appl	
24	595.8	55.6	2464	3	US-08-653-648A-3	Sequence 3, Appli	

Query Match	50.4%;	Score 636.4;	DB 3;	Length 2126;
Best Local Similarity	76.6%;	Pred. No. 6.2e-173;		
Matches 813;	Conservative 0;	Mismatches 231;	Indels 18;	Gaps 2;
Qy	1	CCTGAGTGCTAGTATCCCGAGACTCAGTCGCGCCATGAAGCGGAAGAGAGAAGAACACAG	60	
Db	989	CCCGATGCTGTGGTCCAGAAACCCAGTGTGCGCAAAAGGAAGAGAGAAGAACACAG	1048	
Qy	61	AAGGAGAAGGACAAAATCTGCTTCAGCAACGACGACGGTGGAGACACATGCGCGCCCATTT	120	
Db	1049	AGAGAAAAGACAAAATCTACCAAGTGAGCACAAACGACAGTAGACGATCATATGCCCCCAATC	1108	
Qy	121	ATGCAGGTGTGAACTCTCCACCTCTCTGAAGCAGCAGAGGATTT-----CAGGAA	165	
Db	1109	ATGCAGGTGTGATTCGGCCACCCCGGAGGACGCGAGGATTTCTGNAATGTTTGACGACATGAA	1168	
Qy	166	GTGCTCCCAAGGTTTTCTCTCCGACAACTGTTGGAGACAAACCGGCAGAAAACATCCCC	225	
Db	1169	GTGCTCCCGGGTTTCTCTCGGAGAGCTGATGAGCAGAGATTCGGTTGAAGACATACACC	1328	

Db 1660 GACATGTGCTAGCGCTGCTCACCGCCATGTTATATTTCTCAGACCGGCCAGGCGTCTC 1719
Qy 721 GAGCAGCGCAACTGGTGGAGAAATCCAGCGGTACTACCTGAATACGCTCCGCACTTAT 780
Db 1720 GAGCAACCCCTTTTAGTGGAGAAATCCAGAGATACTACTTTGAAGAGCGCTCGGGTTTAC 1779
Qy 781 ATCTGACAGCTGAGCGGCTCGCGGTTGCTGCGGTTCGTCATATATATATATATATATATAT 840
Db 1780 ATTTTAAATACGACAGCGCGTCTGCTGCGCGGCTGCTGCTGCGCGGCTGCTGCTGCGG 1839
Qy 841 ATCTCTCTGAGCTACGACGCTGCGCATGCAAACTCCAACTGTCATCTCCCTCAAG 900
Db 1840 GTGCTGAGGAACTGCGCACTGCGCACTGCGCACTGCGCACTGCGCACTGCGCACTGCG 1899
Qy 901 CTCAAGAACAGAAAGCTGCGCGCTTTCTCAGAGAGATCTGGGATGTGGCGAGCATGTG 960
Db 1900 CTGAAGAACAGAAACTTCCGCCATTCCTCAGAGAGATCTGGGAGTCTGGGAGTGTGTCG 1959
Qy 961 CACACCCACCGCGCC 977
Db 1960 ACGACGCGCGCGGCC 1976

RESULT 3

US-10-087-167-67.
; Sequence 67, Application US/10087167
; Patent No. 6958236
; GENERAL INFORMATION:
; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; PRIOR FILING DATE: 2002-03-01
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67
; LENGTH: 1500
; TYPE: DNA
; ORGANISM: Synthetic construct
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1500)
; OTHER INFORMATION: Ecdysone Receptor chimera MEV
US-10-087-167-67

Query Match 59.0%; Score 621.6; DB 3; Length 1500;
Best Local Similarity 78.5%; Pred. No. 9.8e-169;
Matches 744; Conservative 0; Mismatches 204; Indels 0; Gaps 0;
Qy 1 CCTGAGTGGCTAGTACCGGAGCTCAGTGGCCCATGAAGCGGAAAGAGAAAGACAG 60
Db 310 CCGAGTGGCTGCTCCAGAGTCCAGCTGCAAGAACAAAGAGAGAGAGAGAGAG 369
Qy 61 AAGAGAGAGCAAACTGCTGTCAGCAAGCAGCGTGGACGACCATGCGCCCAT 120
Db 370 AGAGAAAAGACAACTGCCAGTCCAGTACGACGACAGTGGACGATCATATGCTGCCATA 429
Qy 121 ATGCAAGTGAACCTCCACTCTGAGACGACGAGGATTCAGGAGTGGTCCCAAGTTT 180
Db 430 ATGCAAGTGAACCTCCACTCTGAGACGACGAGGATTCAGGAGTGGTCCCAAGTTT 489
Qy 181 CTCTCCGACAGCTGTTGGAGACAAACCGGACAGAAACATCCCGCTGGACAGCAAC 240
Db 490 CTACGAGAGAGCTAATGAGAGACAGACAGCTGAAGATGTGACGCGCTGTGCGCGAC 549
Qy 241 CAGCAGTCTTATTCGCGAGGCTCATCTGGTACAGGACGCGGTACGAGCAGCTTCTGAT 300
Db 241 CAGCAGTCTTATTCGCGAGGCTCATCTGGTACAGGACGCGGTACGAGCAGCTTCTGAT 300

Db 550 CAGAAGTCCCTGATTCGCGAGGCTGTTGTGTGTAACAGGACGGATACGAGCAGCTTCGGAA 609
Qy 301 GAAGATTTGAAGAGGATTACGACAGCGTGGCAGCAAGCGACGATGAAACGAGAGTCT 360
Db 610 GAGGATCTCAAAAGGGTGCAGCAGCTTGGCAATCAGCAGATGAAGAGAGAGAGACTCA 669
Qy 361 GACACTCCCTTCGCGCAGATCAAGAGATGATATCTCAAGGTCCTTATCTGCTGAG 420
Db 670 GACATGTCATTCGCGCAGATCAAGAAATGACCATCTCAGCTACAGTCAATAGTGTGAG 729
Qy 421 TTGCGGAAGGATTTGCGCAGGTTGCGCAAGATCTCGCAGCTGATCAAAATAGCTCTT 480
Db 730 TTTGCGCAAGGCTTACTGCTGTTTCAAGATCTCAAACTGACCATGATCAATATTA 789
Qy 481 AAGGCTTGTCTCAAGTGAAGTAAATGATCTCCGAGTCCGCGAGCATACGATGCGGCTCA 540
Db 790 AAGGCTGCTCAAGCGAAGTGTGCTGCGAGTAGCGAGGCGGTACGAGCGGTGTCG 849
Qy 541 GACAGTGTCTGTTTCGCGAAACAAAGCGTACACTCGCGACAACTACCGGAAAGGCTGGC 600
Db 850 GATAGCGTCTGTTTCGCGAAACAAAGCGGTACACTCGCGACAACTACCGGAAAGGCGGC 909
Qy 601 ATGCGCTACGTCATCGAGGATCTACGACCTTCTGCGGTCGATGCTACTCTATGCGGTTG 660
Db 910 ATGCGCTACGTCATCGAAGACCTGCTGCACTTCTGCGGCTGCACTGATGCTGATG 969
Qy 661 GACAACTCATTTACGCGCTGCTCAGCGTGTGCTCATCTTTTCTGACCGCGCAGGCTTG 720
Db 970 GACAACTGATTTACGCGCTCTCTCAGTCCCATGTTATTTCTGAGTCCGCGGCTTA 1029
Qy 721 GAGCAGCGCAACTGGTGGAGAAATCCAGCGTACTACCTGAATACGCTCCGCACTAT 780
Db 1030 GAGCAGCGCACTAGTAGAAGAGATCCAGCGGTATTACCTGAAACGCTCGCGGTGTAC 1089
Qy 781 ATCTGACAGCTGAGCGGCTCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
Db 1090 ATCTGACAGCTGAGCGGCTCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1149
Qy 841 ATCTCTCTGAGCTACGACGCTCGCGATCGCGATCAAACTCCAACTGTCATCTGCTCAAG 900
Db 1150 GTGCTTACGAGTGGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCG 1209
Qy 901 CTCAAGAACAGAAAGTGGCGCTTTCTCAGGAGATCTGGGATGTG 948
Db 1210 CTCAAGAACAGAAAGTGGCGGCTTCTGAGGAGATCTGGGAGCTG 1257

RESULT 4

US-10-087-167-120
; Sequence 120, Application US/10087167
; Patent No. 6958236
; GENERAL INFORMATION:
; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; CURRENT FILING DATE: 2002-03-01
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 120
; LENGTH: 1767
; TYPE: DNA
; ORGANISM: Synthetic Construct
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1767)
; OTHER INFORMATION: Ecdysone receptor chimera G(M)EV

US-10-087-167-120

Query Match 59.0%; Score 621.6; DB 3; Length 1767;
Best Local Similarity 78.5%; Pred. No. 16-168;
Matches 744; Conservative 0; Mismatches 204; Indels 0; Gaps 0;

QY 1 CCTGAGTGGCTAGTACCGGAGCTCAGTGGCCATGAAGCGGAAGAAAGAAAGCAG 60
DB 577 CCGAGTGGCTGTCCAGAGTCACTGTCAGAACAAAGAAAGAAAGAAAGCAG 636

QY 61 AAGGAGAGGACAACTGCTGTGACGACGAGCGGTGACGACCAATGCGCCCAT 120
DB 637 AGAGAAAAGCAAACTGCGAGTCACTGACGACGAGTGAAGTATGCTGCGCAT 696

QY 121 ATGCAAGTGAACCTCACTCTGAGGACGAGGATTCACGAGTGGTCCCAAGTTT 180
DB 697 ATGCAATGTGACCTCGCGCCCGAGAGCGGCAAGGATTCACGAGTGGTCCGAGTTT 756

QY 181 CTCTCCGACAAAGCTGTTGGAGACAAACCGGCGAGAAAACATCCCGATGACAGCAAC 240
DB 757 CTAAACGAGAGCTAATGGAGCAGAACAGTGAAGATGTGACGCGCTGTGCGGAAC 816

QY 241 CAGCAGTTCCTTATCGCCAGAGCTCATCTGTTACCGAGAGCGGTACGAGCAGCTTCTGAT 300
DB 817 CAGAGTCTCTGATCGCGAGGCTCGTGTGTACCGAGAGGGGTACGAGCAGCGTGGAG 876

QY 301 GAAGATTGAAGAGGATTAACGAGAGTGGCGAGCAAGCGGACGATGAAGAAAGAGAGTCT 360
DB 877 GAAGATCTCAAGAGAGTATACAGACATGCGAGTGAAGAAAGAAAGAGAGGAACT 936

QY 361 GACACTCCCTTCGCGAGATCAAGAGATCACTATCTCAAGATATCTCAGTCCGATCAATATTA 480
DB 937 GACATGCCCTTCGCTCAGATCAAGAGATGAAGTCTTAACAGTGGAGTCACTTATGAGAA 996

QY 421 TTGCGCAAGGAGTGGCGAGGTTGCGCAAGATCTCGAGCGTGTGATCAAAATACGCTGCTT 480
DB 997 TTGCGCAAGGAGTGGCGAGGTTGCGCAAGATATCTCAGTCCGATCAATATTA 1056

QY 481 AAGGCTTGTCAAGTGAAGTAAATGATGCTCCGAGTGGCGAGATCAAGTATGCGGCTCA 540
DB 1057 AAGGCTCATCAAGCGAAGTGAATGATGCTGCGAGTGGCGAGCGGTACGAGCGGCGAG 1116

QY 541 GACAGTGTCTGTTGCGGACAAACAGAGTGAATCTCTCAAGTGGAGTACCGAGAGGCTGC 600
DB 1117 GACAGGTGTCTGTTGCGGACAAACAGAGGTTACAGCGGATCACTACCGAGAGGCGGC 1176

QY 601 ATGGCTTACGTCAGGATCTACTGCACTTCTGCGGTGCGATGTAATCTATGCGGTG 660
DB 1177 ATGGCTTACGTCAGGATCTACTGCACTTCTGCGGTGCGATGTAATCTATGCGGTG 1236

QY 661 GACAACTCAATTAAGCGCTGCTCAGCGTGTGTGATCTTTTCTGACCGGCGAGGTTG 720
DB 1237 GACAACTGATTAAGCGCTTCTCACTGCCATCGTTATATTTCTGCGATCGCGCGGCTA 1296

QY 721 GAGCAGCGCAACTGTTGGAGAAATCCAGCGGTACTACCTGATATACGCTCCGATCTAT 780
DB 1297 GAGCAGCGCAAGTGTAGAGAGATCCAGCGGTATTAACCTGAAACAGCTCGCGGTTGAT 1356

QY 781 ATCTGAAACAGCTGAGCGGTGCGCGGTTGCTGCTGCTATATACGCGAAGATCTCTCA 840
DB 1357 ATCAATGAACAGCAGCAGCGGTGCGCGGTTGCGCGCTCATCTAAGGAGATCTGTGCG 1416

QY 841 ATCTCTCTGAGCTTACGAGCTGCGATGCAAACTCCAAACATGTCATCTCTCAAG 900
DB 1417 GTGCTTACCGAGTGTGCGAGCGCTGGGATGCGAAATTCGAAATGTGCACTCGCTGAAG 1476

QY 901 CTCAGAACAGAGAGCTGCGCGCTTTCTCTGAGGAGATCTGGGATG 948
DB 1477 CTCAGAACAGAGAGCTGCGCGCTTTCTCTGAGGAGATCTGGGACGTG 1524

RESULT 5

US-10-087-167-136

; Sequence 136, Application US/10087167
; Patent No. 6958236
; GENERAL INFORMATION:
; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 136
; LENGTH: 1863
; TYPE: DNA
; ORGANISM: Synthetic Construct
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1863)
; OTHER INFORMATION: Ecdysone receptor chimera G(M)MD
US-10-087-167-136

Query Match 58.6%; Score 617.4; DB 3; Length 1863;
Best Local Similarity 76.3%; Pred. No. 1.7e-167;
Matches 759; Conservative 0; Mismatches 236; Indels 0; Gaps 0;

QY 1 CCTGAGTGGTGTAGTACCGAGACTCAGTGGCCATGAGCGGAAGAAAGAAAGCAG 60
DB 577 CCGAGTGGTGTGCTCCAGAGTCCAGTGCAGAAACAAAGAAAGAAAGAAAGCAG 636

QY 61 AAGGAGAGGACAACTGCTGTGACGACGAGCGGTGACGACCAATGCGCCCAT 120
DB 637 AGAGAAAAGCAAACTGCGAGTCACTGACGACGAGTGAAGTATGCTGCGCAT 696

QY 121 ATGCAAGTGAACCTTCCACTCTGTAAGCAGCAAGATTCACGAGTGGTCCCAAGTTT 180
DB 697 ATGCAATGTGACCTCGCGCCCGAGAGCGGCAAGGATTCACGAGTGGTCCGAGTTT 756

QY 181 CTCTCCGACAAAGCTGTTGGAGACAAACCGGCGAGAAAACATCCCGATGACAGCAAC 240
DB 757 CTAAACGAGAGCTAATGGAGCAGAACAGTGAAGATGTGACGCGCTGTGCGGAAC 816

QY 241 CAGCAGTTCCTTATCGCCAGAGCTCATCTGTTACCGAGAGCGGTACGAGCAGCTTCTGAT 300
DB 817 CAGAGTCTCTGATCGCGAGGCTCGTGTGTACCGAGAGGGGTACGAGCAGCGTGGAG 876

QY 301 GAAGATTGAAGAGGATTAACGAGAGTGGCGAGCAAGCGGACGATGAAGAAAGAGAGTCT 360
DB 877 GAAGATCTCAAGAGAGTATACAGACATGCGAGTGAAGAAAGAAAGAGAGGAACT 936

QY 361 GACACTCCCTTCGCGAGATCAAGAGATCACTATCTCAAGTGGAGTACCGAGAGGCTGC 420
DB 937 GACATGCCCTTCGCTCAGATCAAGAGATGAAGTCTTAACAGTGGAGTCACTTATGAGAA 996

QY 421 TTGCGCAAGGAGTGGCGAGGTTGCGCAAGATCTCGAGCGTGTGATCAAAATACGCTGCTT 480
DB 997 TTGCGCAAGGAGTGGCGAGGTTGCGCAAGATATCTCAGTCCGATCAATATTA 1056

QY 481 AAGGCTTGTCAAGTGAAGTAAATGATGCTCCGAGTGGCGAGATCAAGTATGCGGCTCA 540
DB 1057 AAGGCTCATCAAGCGAAGTGAATGATGCTGCGAGTGGCGAGCGGTACGAGCGGCGAG 1116

QY 541 GACAGTGTCTGTTGCGGACAAACAGAGTGAATCTCTCAAGTGGAGTACCGAGAGGCTGC 600
DB 1117 GACAGGTGTCTGTTGCGGACAAACAGAGGTTACAGCGGATCACTACCGAGAGGCGGC 1176

QY 601 ATGGCTTACGTCAGGATCTACTGCACTTCTGCGGTGCGATGTAATCTATGCGGTG 660
DB 1177 ATGGCTTACGTCAGGATCTACTGCACTTCTGCGGTGCGATGTAATCTATGCGGTG 1236


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; LENGTH: 1518
; TYPE: DNA
; ORGANISM: Synthetic construct
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1518)
; OTHER INFORMATION: Bcdysone Receptor chimera MMV
US-10-087-167-93

Query Match      58.5%; Score 617; DB 3; Length 1518;
Best Local Similarity 75.7%; Pred. No. 2.le-167;
Matches 764; Conservative 0; Mismatches 245; Indels 0; Gaps 0;

Qy 1 CTTGAGTGCCTAGTATCCCGAGACTCATGTCGCCCATGAAGCGGAAGAGAAGAAGACACAG 60
Db 310 CCCGAGTGCCTGCTCCCGAGATCCCATGTGAAGAACAAAGAAAGAGAAAAGGAAGACACAG 369

Qy 61 AAGGAGAAGACAAAACCTGCTGTGACACACACGAGCGGTGACGACACATATGCCGCCATT 120
Db 370 AGAGAAAAGACAAACTGCGCAGTCAGTACGACGACGTGACGATCATATGCTTGCCONTA 429

Qy 121 ATGCAGTGTGAACTCCCACTCTCTGGAAGCAGCAGAGATTACGAAGTGGTCCCAAGTTT 180
Db 430 ATGCAATGTGACCTCTCCGCCCCAGAGCGCGCAAGGATTCAAGAGTGGTCCCGAGGTT 489

Qy 181 CTCTCCGACAAAGCTGTTGGAGACAAACCGCGGAGAAAACAATCCCCCAGTTGACAGCCAAC 240
Db 490 CTAACGGAGAAGCTTAATGGAGCAGAAACAGACTGGAAGAAATGTGAACGCCGCTGTTCGGCGAAC 549

Qy 241 CAGCAGTTCTTATTCGCGCAGCTCATCTGTTACCAGGACGGGTACGAGCAGCCTTCTGAT 300
Db 550 CAGAAATGCCCTGATTCGCGAGGCTCGTGTGGTACGAGAGGGGTACGAGCAGCGTTCGGAG 609

Qy 301 GAAGATTGAAGAGGATTACGCGACAGCTGGCAGCAGCGGACGATGAAAAACGAAGTCT 360
Db 610 GAAGATCTCAAGAGAGTTACACAGACATGCGCAGTTAGAGAGAAAGAGAGGAGAACT 669

Qy 361 GACACTCCCTTCGCGCAGATCAGAGATGACTATCTCTCAGCGTCCAACTTATCGTGAG 420
Db 670 GACATGCCCTTCGCTCAGATCACAAGATGACGATCTTAAACAGTGCAGCTTATTTGTAGAA 729

Qy 421 TTCGGAAGGATGTCGCAAGGTTTCGCGAAGATCTCGCAGGCTGATCAAAATTAACGCTGCT 480
Db 730 TTCGAAGGACTACCGGATTTCTCCAGATATCTCAGTCCGATCAAAATTAATATTATTA 789

Qy 481 AAGCTTGTCTCAAGTAGGTAATGATGCTCCGAGTCGCGGACGATACGATCGGCGCTCA 540
Db 790 AAGCGTCTATCAAGCGAAGTATGATGCTGCGAGTGGCGGACGCTACGACGCGCGCAGC 849

Qy 541 GACAGTCTTCTGTTTCGCGAACAAACCAAGCGTACACTCGGACAACTACCGCAGGCTGGC 600
Db 850 GACAGCGTCTGTTTCGCGAACAAACCGCGCTGACACGCGCGCAACTACCGCAAGGCGCGC 909

Qy 601 ATGCGCTACGTCACTGAGGATCTACTGCACTTCTGCGGTCGATGTAATCTATGCGCGTGG 660
Db 910 ATGTCTTAAGTCACTGAGGACCTGCTGCACTTCTGTGCGGTGATGTAATCTCATGAGCATG 969

Qy 661 GACAACTATCCATTAAGCGCTGCTCAACGCTGTGCTGATCTTTTCTGACCGGCGCAGGTTG 720
Db 970 GACAAATGTGCACTACGCGCTGCTCAACGCGCATCGTTATATTTCTCAGACCGGCGCAGGCTC 1029

Qy 721 GAGCAGCGGCAACTGGTGGAGAAATCCAGCGGTACTACCTGATGATAAGCTCCGATCTAT 780
Db 1030 GAGCAAAACCCCTTTTATGTTGGAGAAATCCAGAGATACTACTTGAAGACGCTGCGGGTTTAC 1089

Qy 781 ATCTCGAACCACTGAGCGGTCGCGCGTTCGTCCTCATATATACGCAAGATCTCCTCA 840
Db 1090 ATTTTAATCAGCACAGCGGTGCGCTCGCTGCGCGTGTGTTTCGCGAAGATCTCTCGG 1149

Qy 841 ATCTCTCTGAGCTACGCAACGCTCGGATGCAAAATCTCAACATGTGATCTCCCTCAAG 900
Db 1150 GTGCTGACGGAATCTGCGCAACGCTCGGACGCAAGAACTCAACATGTGATCTCGCTGAG 1209

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Qy	901	CTCAAGAACAGAAAGCTGCGCCTTTCTCTCGAGAGATCTGGGATGTGGCGGACATGTGCG	960
Db	1210	CTGAAGAACAGGAAACTTTCGCCATTCTCGAGGAGATCTGGGACGTGGCGGAAAGTGTGCG	1269
Qy	961	CACACCCACCGCGCGCTATCTCTCGAGTCCCCCAGCAATCTCTAGCCCC	1009
Db	1270	ACGACGAAGCTTCCCCCCCCGACCGATGTGAGCTGGGGACGAGTCC	1318
RESULT 8			
US-10-087-167-104			
; Sequence 104, Application US/10087167			
; Patent No. 6958236			
; GENERAL INFORMATION:			
; APPLICANT: Pascal, Erica			
; APPLICANT: Valentine, Scott			
; APPLICANT: Brown, Jeffrey			
; APPLICANT: Cockrell, Adam			
; APPLICANT: Johnson, Brian			
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS			
; FILE REFERENCE: 50018A			
; CURRENT APPLICATION NUMBER: US/10/087,167			
; CURRENT FILING DATE: 2002-03-01			
; PRIOR APPLICATION NUMBER: US 60/242,969			
; PRIOR FILING DATE: 2000-10-24			
; NUMBER OF SEQ ID NOS: 148			
; SOFTWARE: Patent in version 3.1			
; SEQ ID NO 104			
; LENGTH: 3972			
; TYPE: DNA			
; ORGANISM: synthetic construct			
; FEATURE:			
; NAME/KEY: misc feature			
; LOCATION: (1)..(3972)			
; OTHER INFORMATION: GAL4-Manduca EcR-VP16 fragment in pGSG202			
; NAME/KEY: CDS			
; LOCATION: (2007)..(3668)			
; OTHER INFORMATION: GAL4-Manduca EcR-VP16 chimera			
US-10-087-167-104			
Query Match 58.5%; Score 617; DB 3; Length 3972;			
Best Local Similarity 75.7%; Pred. No. 3.1e-167;			
Matches 764; Conservative 0; Mismatches 245; Indels 0; Gaps 0;			
Qy	1	CCTGAGTGCCTAGTACCAGAGACTCAGTGCCTATGAAGCGGAAGAGAGAAAGACACAG	60
Db	2460	CCCGAGTGCCTGCTGCCAGAGTCCAGTGCAGCAACAAAAGAGAGAAAAGGAGACACAG	2519
Qy	61	AAGAGAGAGACAAAACCTGCCTGTGCAGCAACGACGAGTGCAGCACCATATGCCCGCCCAT	120
Db	2520	AGAGAAAAGCAAACTGCCAGTCAGTACGACGACAGTGAACGATCATATGCCCTGCCATA	2579
Qy	121	ATGCAGTGTGAACTTCACTCTCTGAAGCAGCAGAGGATTCACGAAGTGTGTCGAAGTTT	180
Db	2580	ATGCAATGTGACCTTCGCGCCCCAGAGCGCGCAAGGATTCACGAAGTGTGTCGAGGTTT	2639
Qy	181	CTCTCCGACAGCTGTTGGAGACAAACCGGACAGAAAACATCCCCAGTTGACAGCCAAC	240
Db	2640	CTAACGGAGAGCTTAATGGAGCAGAAACAGACTGAAGAATGTGACGCGCTGTTCGGCGAAC	2699
Qy	241	CAGCAGTTCCTTATTCGCGCAGGCTCATCTGGTACCAGGACGGGTACGACGAGCCCTTCTGAT	300
Db	2700	CAGAAGTCCCTGATCGGAGGCTCGTGTGGTACGAGGAGGGGTACGAGCAGCCGTCGGAG	2759
Qy	301	GAAGATTGAGAGGATTATCGCAGACTGGCAGCAGCGGACGATGAAAAACGAAGAGTCT	360
Db	2760	GAGATCTCAAGAGAGTTACACAGCATGGCAGTTAGAGAAAGAAAGAGGAGGAAACT	2819
Qy	361	GACACTCCCTTCGCGCAGATCAGAGATGCACTATCTCAAGTCCCACTTATCTGTCGAG	420
Db	2820	GACATGCCCTTCGCTCAGATCACAGATGACGATCTTAAACGTCGAGCTTATTGTAGAA	2879
Qy	421	TTCCGGAAGGGAATTGCCAGGGGTTCCGCAAGATCTTCGACGCGCTGATCAAAATTAACGCTCCT	480


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; GENERAL INFORMATION:
; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 142
; LENGTH: 1809
; TYPE: DNA
; ORGANISM: Synthetic Construct
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1809)
; OTHER INFORMATION: Ecdysone receptor chimera VG(M)M
; US-10-087-167-142

Query Match      58.5%; Score 616.4; DB 3; Length 1809;
Best Local Similarity 77.2%; Pred. No. 3.3e-167;
Matches 749; Conservative 0; Mismatches 221; Indels 0; Gaps 0;

QY 1 CTTGAGTGGCTAGTACCCGAGACTCAGTGGCCATGAAGCGGAAAGAGAAAGACACAG 60
DB 835 CCGAGTGGCTGGTCCGAGAGTCCAGCTGCACGAAACAAAGAGAGAAAGAGACACAG 894
QY 61 AAGGAGAGACAAACTGCTCTGACGACGACGACGACGACGACGACGACGACGACGACG 120
DB 895 AGAGAAAGACAAACTGCCAGTCCAGTACGACGACGACGACGACGACGACGACGACG 954
QY 121 ATGCAGTGTGAACCTCCAGCTCTGAGAGCAAAACCGGAGAGAGAGAGAGAGAGAG 180
DB 955 ATGCAGTGTGAACCTCCAGCTCTGAGAGCAAAACCGGAGAGAGAGAGAGAGAGAG 1014
QY 181 CTCTCGACAGCTGTTGGAGACAAACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
DB 1015 CTAACGGAGAGAGCTAATGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1074
QY 241 CAGCAGTGTCTTATCGCCAGGCTCATCTGGTACAGAGCGGGTACGAGAGAGAGAGAG 300
DB 1075 CAGAAGTCCCTGATCGCGAGGCTGCTGGTACAGAGAGAGAGAGAGAGAGAGAGAGAG 1134
QY 301 GAAGATTTGAAGAGATTACGAGAGCTGCGAGAGCTGCGAGAGAGAGAGAGAGAGAG 360
DB 1135 GAAGATTTGAAGAGATTACGAGAGCTGCGAGAGCTGCGAGAGAGAGAGAGAGAGAG 1194
QY 361 GACATCCCTTCCGACAGATCAGAGAGATGACTATCTCCAGGTCCAACTTATCGTGGAG 420
DB 1195 GACATCCCTTCCGACAGATCAGAGAGATGACTATCTCCAGGTCCAACTTATCGTGGAG 1254
QY 421 TTCCGAGAGGATTTGCCAGAGGTTGCCAGAGATCTCGCAGAGCTGATCAAAATACGCTGT 480
DB 1255 TTCCGAGAGGATTTGCCAGAGGTTGCCAGAGATCTCGCAGAGCTGATCAAAATACGCTGT 1314
QY 481 AAGGCTTGTCTCAAGTGAAGTAAATGATCTCCAGTTCGCGAGAGAGAGAGAGAGAGAG 540
DB 1315 AAGGCTTGTCTCAAGTGAAGTAAATGATCTCCAGTTCGCGAGAGAGAGAGAGAGAGAG 1374
QY 541 GACAGTGTCTTGTTCGGGAAACAAACAGCGGTACACTCGGACAACTACCGCAAGGCTGGC 600
DB 1375 GACAGTGTCTTGTTCGGGAAACAAACAGCGGTACACTCGGACAACTACCGCAAGGCTGGC 1434
QY 601 ATGGCCCTACGTACAGAGGATCTACTGCACTTCTCGCGGTGCGATGATCTATGGCGTTG 660
DB 1435 ATGGCCCTACGTACAGAGGATCTACTGCACTTCTCGCGGTGCGATGATCTATGGCGTTG 1494
QY 661 GACAAACATCCATACGCGCTGCTCAGCGCTGTGCTCATCTTTTCTGACCGGCGAGGTTG 720

; US-10-087-167-75
; Sequence 75, Application US/10087167
; Patent No. 6958236
; GENERAL INFORMATION:
; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 75
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Synthetic construct
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1515)
; OTHER INFORMATION: Ecdysone Receptor chimera REV
; US-10-087-167-75

Query Match      58.3%; Score 614.2; DB 3; Length 1515;
Best Local Similarity 78.4%; Pred. No. 1.3e-166;
Matches 755; Conservative 0; Mismatches 193; Indels 15; Gaps 1;

QY 1 CTTGAGTGGCTAGTACCCGAGACTCAGTGGCCATGAAGCGGAAAGAGAAAGACACAG 60
DB 310 CCGAGTGGCTGGTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 369
QY 61 AAGGAGAGAGACAAACTGCTCTGACGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
DB 370 AAGGAGAGAGACAAACTGCTCTGACGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 429
QY 121 ATGCAGTGTGAACCTCCAGCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 165
DB 430 ATGCAGTGTGAACCTCCAGCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 489
QY 166 GTGGTCCCAAGGTTTCTCTCGGACAAAGCTGTTGGAGACAAACCGGAGAGAGAGAGAG 225
DB 490 GTGGTCCCAAGGTTTCTCTCGGAGAGAGCTGATGGAGAGAGAGAGAGAGAGAGAGAGAG 549
QY 226 CAGTTGACAGAGCAACCAAGCAGTGTCTTATCGCGAGGCTCATCTGTTACGAGGAGGTTAC 285
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Db 550 CCCCCTCACCGCCCAACAGCAGTTCCTGATCCGAGGCTGGTGTGATCCAGGACGGATAC 609
Qy 286 GAGCAGCGCTTCTGATGAAGATTTTGAAGAGGATTAACGACAGCTGGCGAGCAAGCGGACGAT 345
Db 610 GAGCAGCGCTTCCGGAAGAGGATCTCAAAAGGGTGAACGAGCTTGGCAATCAGCAGATGAA 669
Qy 346 GAAACAGAGAGTCTGACATCTCCCTTCGCGCAGATCAAGAGATGATATCTCTCACGGTC 405
Db 670 GAAGCAGAGACTCAGACATGCCATTCGCGCAGATCAAGAAATGACCATCTCACAGTA 729
Qy 406 CAACCTATCTGGAGTTCCGCAAGGGATTCGAGGTTCCGAGAGATCTGCGACCTGAT 465
Db 730 CAGCTAATAGTCGAGTTTCCCAAAGGCTACCTGGTTTTTCAAGATCTCACACCTGAC 789
Qy 466 CAAATTACCGCTGCTTAAGGCTTGTCAAGTGAGGTAATGATGCTCCGAGTCCGCGCAGCA 525
Db 790 CAGATCACATATTAAAGGCATGCTCAAGCGAAGTATGATGCTGCGAGTAGCGAGCGG 849
Qy 526 TAGCATCGGCGCTCAGACAGTGTCTGTTCCGCAACCAACCAAGGTTACATTCGCGCAAC 585
Db 850 TACGACGCGGTGTCGATAGCGTTCTGTTGCCCAACCAACCAAGGCTACATTCGCGCAAC 909
Qy 586 TACGCAAGGCTGCGATGCGCTACGTCATCGAGGATCTACGCACTTCTGCGGTGCAATG 645
Db 910 TACGCAAGGCTGCGATGCGCTACGTCATCGAAGACCTGCTGCACTTCTGCGGTGCAATG 969
Qy 646 TACTCTATGGCGTTGGACAACATCCATTACGCGTGTCTACGCGTGTGCTGATCTTTTCT 705
Db 970 TACTCGATGTCGATGGAACAGTGCTATACGCGTCTCTACTGCGCATGTTATATTCG 1029
Qy 706 GACCGCGCGGTTGGAGCAGCGCCCAACTGTTGGAAGAAATCCAGCGGTACTACCTGAAT 765
Db 1030 GATCGCGCGGCTTAGAGAGCCACAGCTAGTAGAAGAGATCCAGCGGTATTACCTGAAC 1089
Qy 766 ACGTCCGCACTATATCTCTGAACAGCTGAGCGGTCGCGGCTTCTGCTGCTCATATAC 825
Db 1090 ACGTTCGCGGTTGATCATATGAACAGCAGCAGCGCGTTCGCGGCTTCTGCGGTCTATC 1149
Qy 826 GGCAAGATCTCTCAATCTCTCTGAGTACGACGCTGCGCATGCAAAATCTCAACATG 885
Db 1150 GCGAAGATCTCTGCGGTCTTACGAGTTGCGGACGCTGCGCATGCAAGATTCGAATG 1209
Qy 886 TGCACTCTCCCTCAAGCTCAAGAAAGCTGCGCGCTTTCTCTCGAGGAGATCTGGGAT 945
Db 1210 TGCACTCTCGTGAAGCTCAAGAAAGCTGCGCGCTTCTCTCGAGGAGATCTGGGAC 1269
Qy 946 GTG 948
Db 1270 GTG 1272

RESULT 12
US-10-087-167-124
; Sequence 124, Application US/10087167
; Patent No. 6958236
; GENERAL INFORMATION:
; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 124
; LENGTH: 1782
; TYPE: DNA

; ORGANISM: Synthetic Construct
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1782)
; OTHER INFORMATION: Ecdysone receptor chimera G(B)EV
US-10-087-167-124

Query Match 58.3%; Score 614.2; DB 3; Length 1782;
Best Local Similarity 78.4%; Pred. No. 1.4e-166;
Matches 755; Conservative 0; Mismatches 193; Indels 15; Gaps 1;

Qy 1 CCTGAGTGGTGTAGTACCCGAGACTCAGTGGCCATGAGCGGGAAGAGAGAGCAAGCAG 60
Db 577 CCCGAGTGGTGTGCGAGAAACGCGAGTGTGCGCAAAAGGAAGAGAGAAAGCAG 636
Qy 61 AAGGAGAGAGCAAAATGCTCTGTGAGCAGCAGCAGCGTGGACACACACATCGCCGCAAT 120
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Qy 121 ATGCAGTGGAACCTCCACTCTCTGAAAGCAAGGAT-----CACGAA 165
Db 697 ATGCAGTGTGATCCACCAACCCCGAGGAGCGAGGATTTCTGGAATGTTTGCAGCATGAA 756
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Qy 886 TGCACTCTCCCTCAAGCTCAAGAAAGCTGCGCGCTTTCTCTCGAGGAGATCTCGGAT 945

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Qy 181 CTCTCCGCAAGCTGTTGGAGACAACCGCGAGAAAAACATCCCCAGTTGACAGCCAAAC 240
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Db 1234 GATTAAGTGCACTACGCGCTCTTACGCGCATGTGCTATTTCTCAGACCGGCTTGGGCTC 1293
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Db 1474 CTGAAGATAGGAGCTGCGCGCTTCTCTCAGGAGATCTGGGAGTGG 1522

RESULT 15

US-10-087-167-79
; Sequence 79, Application US/10087167
; Patent No. 6958236
; GENERAL INFORMATION:
; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 79
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Synthetic construct
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1533)
; OTHER INFORMATION: Ecdysone Receptor chimera EMV
US-10-087-167-79

Query Match 57.8%; Score 609.6; DB 3; Length 1533;
Best Local Similarity 75.7%; Pred. No. 2.8e-165;
Matches 775; Conservative 0; Mismatches 234; Indels 15; Gaps 1;
Qy 1 CCTGAGTGCCTAGTACCCGAGACTCACTGAGTGCCTATGAAGCGGAGAAAGAAAGCAAG 60
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Db 370 AGAGAAAAAGCAAACTTACCAAGTGAGCAACAACGACAGTAGACGATCATATGCCCCCAATC 429
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Qy 166 GTGCTCCCAAGGTTTCTCTCCGACAAAGCTGTTGGAGACAAACCGGAGAAAAAATCATCCCC 225
Db 490 GTGCTCCCGGGTTCTCTCGGAGAGCTGATGGAGCAGATCGGCTGAAGAACATATACC 549
Qy 226 CAGTTGACAGCAACCAAGGTTCTTATGCGCAGGCTCATCTGGTACAGAGCGGGTAC 285
Db 550 CCCTTCAACCCCAACCAAGGTTCTTATGCGCAGGCTGCTGCTGAGTACCAAGGAGGGGTAC 609
Qy 286 GAGCAGCTTCTGATGAAGATTTGAAGAGGATTAACGACAGCTGGCAGCAAGCGGAGAT 345
Db 610 GAGCAGCGCTCGGAGGAGATCTCAAGAGAGTTTACAGACATGGCGAGTTAGAAAGAA 669
Qy 346 GAAAAAGAGAGTCTGACACTCCCTTCCGACAGATCAAGAGATGACTATCTCACCGTTC 405
Db 670 GAAGGAGGAGAACTGACATGCCCTTCCGTCAGATCAAGAGATGAGCATTTAAACAGTG 729
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Qy 766 ACCTTCGCGCATCTATATCTTGAACAGCTGAGCGGTCGCGCGTTCGCTCGGTATATAC 825
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Qy	886	TGCATCTCCCTCAAGCTCAAGAACAGAAAGCTGCGGCTTTCTCTCGAGGAGATCTGGAT	945
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Db	1330	CTCC 1333	

Search completed: January 31, 2006, 14:11:00
Job time : 236 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 31, 2006, 09:09:55 ; Search time 4078 Seconds
(without alignments)

12092.591 Million cell updates/sec

Title: US-09-965-703A-3

Perfect score: 1054

Sequence: 1 cctgagtcgtagtaccgca.....gtccggccgcgtctctga 1054

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: gb_est1.*
2: gb_est2.*
3: gb_est3.*
4: gb_est4.*
5: gb_est5.*
6: gb_est6.*
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8: gb_est8.*
9: gb_est9.*
10: gb_est10.*
11: gb_est11.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	314.2	29.8	963	4	CNS0905M
2	233.6	24.1	728	3	BM650826
3	231.4	22.0	851	10	CNS01IME
4	200.8	19.1	470	1	AA538642
5	151.6	14.4	574	1	A1258616
6	146.2	13.9	1050	10	CNS016YX
7	130	12.3	1088	5	BA463524
8	127.6	12.1	867	3	BQ222200
9	127	12.0	1031	3	BQ058428
10	125.6	11.9	1963	4	AK077620
11	125.4	11.9	651	7	CN309352
12	125.4	11.9	667	6	CD673041
13	125.4	11.9	918	3	BQ214241
14	125.4	11.9	1386	11	DQ052757
15	125.4	11.9	1685	4	CR614375
16	125.4	11.9	1763	4	CR610600
17	125.4	11.9	1828	4	CR617823
18	125.4	11.9	1922	4	CR604070
19	125.4	11.9	1924	4	CR609885
20	125.4	11.9	1965	4	CR598124
21	125.4	11.9	1978	4	CR598123
22	125.2	11.9	1190	11	DQ052758

23	124	11.8	721	2	BE382387	BE382387	601298693
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25	119	11.3	2035	4	CR749648	Homo sapi	CR749648
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27	116.2	11.0	986	5	BQ877581	AGENCOURT	BQ877581
c	28	115	10.9	792	7	CR996932	CR996932
c	29	115	10.9	1062	5	EX367164	EX367164
c	30	114.8	10.9	920	1	AL522738	AL522738
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c	34	114	10.8	1003	5	EX344136	EX344136
c	35	112.6	10.7	1933	4	CR857510	CR857510
c	36	112.4	10.7	1135	5	EX365740	EX365740
c	37	112.2	10.6	779	2	BE391856	BE391856
c	38	111.2	10.6	755	8	DN548627	DN548627
c	39	111.2	10.6	1026	3	BQ052341	BQ052341
c	40	109.4	10.4	622	5	BQ636916	BQ636916
c	41	108.8	10.3	679	3	BM716607	BM716607
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ALIGNMENTS

RESULT 1	CNS0905M	963 bp	mrna	linear	HTC 22-APR-2005
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ACCSSION	EX067382	GI:27640663			
VERSION	EX067382.1	GI:27640663			
KEYWORDS	HTC				
SOURCE	Anopheles gambiae (African malaria mosquito)				
ORGANISM	Anopheles gambiae				
REFERENCE	1				
AUTHORS	Gomez, S.M., Eglmeier, K., Segreus, B., Dehoux, P., Couloux, A., Scarpetti, C., Wincker, P., Weissenbach, J., Brey, P.T. and Roth, C.W.				
TITLE	Pilot Anopheles gambiae full-length cDNA study: sequencing and initial characterization of 35,575 clones				
JOURNAL	Genome Biol. 6 (4), R39 (2005)				
PUBMED	15833126				
REFERENCE	2	(bases 1 to 963)			
AUTHORS	Genoscope				
TITLE	Direct Submission				
JOURNAL	Submitted (06-JAN-2003) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr)				
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Best Local Similarity	72.4%	Pred. No. 7.9e-75;			
Matches	435;	Conservative	0;	Mismatches 163;	Indels 3;
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Db 9 GAAATCCACTTCGCGCATACATACGAAATCACCATCTCCACAGTACACAACTAATCGTCGAG 68
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 Db 428 ATCTGAAACAGCTGAGCGGTCGCGGCTGCTGCGTATATACGCGCAAGATCCTCTCA 885
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 Db 606 C 606

RESULT 2
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 LOCUS 1700687372602 A.Gam.ad.cdna1 Anopheles gambiae cDNA clone
 DEFINITION 19600449637314 5', mRNA sequence.

ACCESSION BM650826
 VERSION BM650826.1 GI:18950337
 KEYWORDS EST.
 SOURCE Anopheles gambiae (African malaria mosquito)
 ORGANISM Anopheles gambiae

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
 Culicidae; Anophelinae; Anopheles.

1 (bases 1 to 728)
 Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L.,
 Charlab,R., Collins,F.H., Venter,J.C. and Hoffman,S.L.
 Celera Anopheles gambiae EST project
 Unpublished (2002)
 CONTACT: Holt R.A.
 Celera Genomics
 45 W. Gude Dr., Rockville, MD 20850, USA
 Tel: 2404533151
 Fax: 2404534580
 Email: HoltRA@celera.com
 Plate: N001004AT row: E column: 24
 Seq primer: M13 Reverse.

1. 728
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FEATURES
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 /mol_type="mRNA"

/strain="RSP-ST (Reduced susc. to Permethrin - std. chromosome)"
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 /clone="19600449637314"
 /dev_stage="Adult"
 /lab_host="DH10b"
 /clone_lib="A.Gam.ad.cdna1"
 /note="Vector: pSport1; Site 1: SalI; Site 2: NotI; Whole adult mosquitoes (mixed sex) frozen on liquid nitrogen. cDNA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3'. Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mr4.org)."

ORIGIN

Query Match 24.1%; Score 253.6; DB 3; Length 728;
 Best Local Similarity 66.3%; Pred. No. 3.2e-58;
 Matches 418; Conservative 0; Mismatches 194; Indels 18; Gaps 3;
 QY 1 CTGTAGTGGTGTAGTACCGAGACTAGTCCGCGCATGAGCGGAAGAGAGAAAGACACAG 60
 Db 105 CCGGAGTGGCTGTGCGGAGAAATCAGTCCGCGCATCAGCGGAAGAGAGAAAGCGCGAG 164
 QY 61 AAGGAGAGGACAACTGCTCTGTAGCAGCAGCAGC-----GGTGGACGACCATGTC 112
 Db 165 AAGGAGAGGACAACTGCTCTGTAGCAGCAGCAGC-----GGTGGACGACCATGTC 224
 QY 113 CGCCCATTTATGAGTGTGAACTCCACCTCTCGAAGCAGCAAGGAT----TCACGAAGTG 168
 Db 225 AGCAGCTACAAGTTCGAGCTGCTGCGGTGCTGATGATGATTCACCGCCACCGCC 284
 QY 169 GTCCCAAGGTTTCTCTCCGACAAAGCTGTGAGAGACAAACCGGAGAAACATCCCCAG 228
 Db 285 GCGATACCGCTACTGCGGAGAAAGCTGTGAAACGAAACCGCAAAAGAAACATACCTCTG 344
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 QY 589 CGCAAGCTGCGCATGGCTTACGTCATCGAG 618
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RESULT 3

CNS011ME

LOCUS

DEFINITION

Accession
 Version
 Keywords

CNS011ME 851 bp DNA linear GSS 26-JUL-1999
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 BACN06K02 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
 AL100448
 AL100448.1 GI:5612059
 GSS.

SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 851)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenosco.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (ADGP) -
http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billaud at CEPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBelobAC11.

FEATURES
source Location/Qualifiers
1..851
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BAC08K02"
/clone_lib="DrosBAC"
/plasmid="pBelobAC11"
/note="end : SP6"

ORIGIN
Query Match 22.0%; Score 231.4; DB 10; Length 851;
Best Local Similarity 65.9%; Pred. No. 4.2e-52;
Matches 351; Conservative 0; Mismatches 181; Indels 1; Gaps 1;
Qy 478 CTTAAGGCTTCTCAAGTGAATGATGCTCCGAGTCGCGACGATGATGCGGCC 537
Db 262 CGTTAGGCTTCTCGTCGAGGTGATGATGCTGCGATGCGACGCTATGACACAGC 321
Qy 538 TCAGACAGTGTCTGTTCCGCAACCAACGCTACACTCCGCAACACTACCGAAGCT 597
Db 322 TCGACTCAATTTCTTCGCAATTAATAGATCATATAGCGGGATTTTACAAATGGCC 381
Qy 598 GGCATGGCTTACGTATGAGGATTTACTGCATTTCTGCGGTGCATGTTCTATGGCG 657
Db 382 GCAATGGCTGATAACATTAAGACCTGCTGCAATTTCTGCCGCCAAATGTTCTCGATGAAG 441
Qy 658 TTGACACATCCATTAGCGCTGCTCAGCGCTGTGTCATCTTTCTGACCGGCCAGGG 717
Db 442 GTGACCAACGTCGAATAGCGCTTCTCACTGCCATTTGTGATCTTTCTCGGACCGCGGCC 501
Qy 718 TTGGAGCAGCGCAACTGGTGGAGAAATCCAGCGGTACTACCTGAATACGCTCGCATC 777
Db 502 CTGGAGAGCGCCAACTAGTCGAGCGNTCCAGAGCTACTACATCGACAGCTAGCATTT 561
Qy 778 TATATCTGAACACAGCTGAGCGGTTCGCGCGTTCGTCGCTCATATATACGCAAGATCCTC 837
Db 562 TATATCTCAACCGCACTGCGGACCTCAATGAGCCT-CGTCTTCTACGCAAGCTGCTC 620
Qy 838 TCAATCTCTCTGAGCTACGACGCTCGGATGCAAACTCCAACTCAATGTCATCTCCCTC 897
Db 621 TCGATCTCTACCGAGCTGCGTACGTCGGCAACAGAACCGCGGATGTGTTTCTCACTA 680
Qy 898 AAGCTCAAGAACAGAAAGCTCCGCTTTCTCGAGGAGATCTGGATGTGGCGGACATG 957
Db 681 AAGTCTCAAAACCGCAACTGCCCAAGTTCTCGAGGAGATCTGGAGGTTTCATGCCATC 740
Qy 958 TCGCACACCCCAACCGCGCTTATCTCTCGAGTCCCGCAAGATCTCTAGCCCTC 1010
Db 741 CCGCCATCGTCCAGTCCGACCTTTCAGATTACCCAGGAGGAGACGAGGCTCT 793

RESULT 4
AA538642

LOCUS AA538642 470 bp mRNA linear EST 19-APR-2001
DEFINITION LD18219.5prime LD Drosophila melanogaster embryo BlueScript
Drosophila melanogaster cDNA clone LD18219 5prime similar to
M74078: Drosophila melanogaster ecdysone receptor (EcR) mRNA,
complete cds, mRNA sequence.
ACCESSION AA538642 GI:2285158
VERSION AA538642.1
KEYWORDS EST.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 470)
AUTHORS Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,
Lewis, S. and Rubin, G.M.
TITLE BGP/HEMI Drosophila EST Project
JOURNAL Unpublished (2001)
COMMENT Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Plate: 182 row: B column: 7
High quality sequence stop: 343.
FEATURES
source Location/Qualifiers
1..470
/organism="Drosophila melanogaster"
/mol_type="mRNA"
/db_xref="BDGP_EST:BDc1n017358"
/db_xref="taxon:7227"
/clone="LD18219"
/sex="male and female"
/dev_stage="0 to 24 hours mixed stage embryonic"
/lab_host="SOLR"
/clone_lib="LD Drosophila melanogaster embryo BlueScript"
/note="Organ: embryo; Vector: BlueScript SK; Site 1:
EcR1; Site 2: XhoI; Constructed using Stratagene ZAP-cDNA
Synthesis kit. Oligo dt-primed and directionally cloned at
EcR1 and XhoI in Bluescript SK(+/-)"
ORIGIN
Query Match 19.1%; Score 200.8; DB 1; Length 470;
Best Local Similarity 65.3%; Pred. No. 9.2e-44;
Matches 295; Conservative 0; Mismatches 157; Indels 0; Gaps 0;
Qy 559 AACACCAAGCGTACACTCGCGCAACTACCGAAGCTGGCATGGCTACGTCATCGAG 618
Db 1 AATAATAGATCATATACCGGGATTTCTTACAAATGGCCGAATGGCTGATAACATTGAA 60
Qy 619 GATCTACTGCACTTCTGCGGTGCATGCTCTATGCGGTGGACACATCCATTACGCG 678
Db 61 GACCTGCTGATTTCTGCGCGCAAAATGTTCTCGATGAAGGTGGACACGTCGAATACGCG 120
Qy 679 CTGCTCAAGCGGTGCTGTCATCTTTCTGACCGCGCCAGGTTGGAGCAGCGCACTCGTG 738
Db 121 CTCTCTACCTGCCATTGGATCTTCTCGACCGCGCGGCTCGGAAGGCTTAATAGTC 180
Qy 739 GAAGAAATCCAGCGGTACTACCTGAATACGCTCGCATCTATATCTCTGAACCGAGCTGAGC 798
Db 181 GAAGCGATCCAGAGCTACTACATCGACACGCTACGCAATTTATATCTCAACCGCACTGC 240
Qy 799 GGGTCGGCGGTTTCGTCGTCATATACGCGCAAGATCTCTCAATCTCTCTGAGCTACGC 858
Db 241 GCGACTCAATGAGCTTCGCTCTTCTAGCAAGGCTGCTCTCGATCTCTCACCGAGCTCGT 300
Qy 859 ACGCTCGGCTACCAAACTCCAACTGTGTCATCTCCCTCAAGCTCAAGAACAGAAAGCTG 918
Db 301 ACGCTGGCAACCAAGACGCGGAGATGTGTTTCTCACTAAGCTCAAAACCGCAACTG 360
Qy 919 CCGCTTTCTCTGAGGAGATCTCGGATGTGCGGACATGTGCGACACCCACCGCGCCT 978


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Db      361  CCCAAGTTCCTCGAGGAGATCTGGGAGTTCATGCCATCCGCCATCGGTCCAGTCGCAC 420
QY      979  ATCTCGAGTCCCCACGATCTCTAGCCCT 1010
Db      421  CTTGAGATTACCCAGGAGGAGACGAGCGTCT 452

RESULT 5
LOCUS   A1258616
DEFINITION
Drosophila melanogaster cDNA clone LP01848 5prime similar to
M74078; Ecr FBgn000546 PID:g157318 SWISS-PROT:P34021, mRNA
sequence.
ACCESSION A1258616
VERSION A1258616.1 GI:3866141
SOURCE EST.
ORGANISM Drosophila melanogaster (fruit fly)
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 574)
REFERENCE Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
AUTHORS Lewis,S. and Rubin,G.M.
TITLE BDGP/HMI Drosophila EST Project
JOURNAL Unpublished (2001)
COMMENT Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd. Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic sequence DS05325
Plate: 18 row: D column: 12
High quality sequence stop: 533.
FEATURES             source
1..574
    /organism="Drosophila melanogaster"
    /mol_type="mRNA"
    /db_xref="taxon:7227"
    /clone="LP01848"
    /sex="male and female"
    /dev_stage="larvae-pupae"
    /lab_hosts="DMS-alpha"
    /clone_lib="LP Drosophila melanogaster larval-early pupal
    pot2"
    /note="Organ: whole body; Vector: pot2; Site 1: EcoRI;
    Site 2: XhoI; Sized fractionated cDNAs were directly
    ligated into pot2. Plasmid cDNA library."

ORIGIN
Query Match      14.4%; Score 151.6; DB 1; Length 574;
Best Local Similarity 60.0%; Pred. No. 3.1e-30;
Matches 275; Conservative 0; Mismatches 174; Indels 9; Gaps 1;

QY      177  GTTTCCTCCGACAAAGCTGTGGAGACAACCCGCGAGAAAACATCCCCAGTTGACAGC 236
Db      126  GCTACTACCTGATGAATAATTGGCCAAGTGTCGAAGCGGCAATATACCTCTTAAAGTA 185
QY      237  CAACGAGAGTTCCTTATCGCAGGCTCATCTGTGTACGAGACGGGTACGAGGAGCTTC 296
Db      186  CAATCAGTTGGCCGTATATACAAGTTAAATTGGTACGAGATGGCTATGACGAGCCATC 245
QY      297  TGATGAAGATTGAAGAGGATTACGACAGCTGGCAGCGGACGATGAACACGAAGA 356
Db      246  TGAAGAGGATCTCAGGCGTATAATGAGT-----CAACCGATGAGAACGAGACCA 296
QY      357  GTCTGACACTCCCTTCGCGCAGATCAAGAGACTATCTCTACGFTCCAACTTATCGT 416
Db      297  AACGAGCGTCAGCTTTCGGCATATAACCGAGATAACCACTACACGGTCCAGTTGATTGT 356

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QY      417  GGAGTTCGGAAAGGATTGCCAGGTTGCCAAGATCTCGCAGCTGATCAAAATTACGCT 476
Db      357  TGAAGTTTCTAAAGTCTACCAAGCGTTTACAAGAATACCCAGGAGACCAATCACGTT 416
QY      477  GCTTAAGGCTTGCTCAAGTGAAGTAATGATGCTCCGAGTCCGCGCAGCATATCGATGCGGC 536
Db      417  ACTAAAGGCTGCTGCTCGGAGGTGATGATGCTGCGATGCGACGACGCTATGACCACAG 476
QY      537  CTCAGACAGTGTCTGTTTCGGAACAACAACGAGGTACACTCCGCGACAATACCGAAGGC 596
Db      477  CTCGGACTCAATATCTTTCGCGAATAATAGATCATATACGCGGATTTCTTACAAAATGCG 536
QY      597  TGCATGGCCTACGTCATCGAGGATCTACTGCACTTCT 634
Db      537  CGAATGGCTGATACATTTGAAGACCTGCTGCACTTCT 574

RESULT 6
LOCUS   CNS016YX
DEFINITION
Drosophila melanogaster genome survey sequence SP6 end of BAC
BACN17G18 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION AL107379
VERSION AL107379.1 GI:5627062
KEYWORDS Drosophila melanogaster (fruit fly)
SOURCE Drosophila melanogaster
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1050)
REFERENCE Genoscope.
AUTHORS Direct Submission
TITLE Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila genome Project (EDGP) -
http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billaud at CEPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBelobAC11.
FEATURES             Location/Qualifiers
1..1050
    /organism="Drosophila melanogaster"
    /mol_type="genomic DNA"
    /db_xref="taxon:7227"
    /clone="BACN17G18"
    /clone_lib="DrosBAC"
    /plasmid="pBelobAC11"
    /note="end : SP6"

ORIGIN
Query Match      13.9%; Score 146.2; DB 10; Length 1050;
Best Local Similarity 51.6%; Pred. No. 1.1e-28;
Matches 249; Conservative 1; Mismatches 230; Indels 3; Gaps 2;

QY      478  CTTAAGGCTTGCTCAAGTGAAGTAATGATGCTCCGAGTCCGCGACGATACGATGCGGC 537
Db      384  CGTTAGGCTTGCTGCTCGGAGGTGNTGCTGCTGCTGTCGCGACGATGNCACAGC 443
QY      538  TCAGACAGTGTCTGTTTCGCGAACAACCAAGCGGTACACTCCGCGACAACCTACCGCAAGGCT 597
Db      444  TCGACTCCTNTTCTTCGCGNTNTAGTCTNTNTTCGCGGGTCTTNCANATGGCC 503
QY      598  GGCATGGCCTTACGTATCGAGGATCTACTGCACTTCTGCGGGTGCATGTACTCTATGGCG 657
Db      504  GGAATGGCTGNTAAACATTGNAGACCTGCTGCTGCTGCTGCGCCNNNTGTTCTCGTGNNG 563
QY      658  TTGACACAACATCCATTACGCGCTGCTCACGGCTGTGTCATCTTTTCTGACCGGCCAGGG 717

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Db      564 GTGNNCGTCGNATNGCCCTTCTCNCCTGCCATTTGNTCTTCTCGNCGGCCGCG 623
Qy      718 TTGAGCAGCGCGCAACTGGTGGAGAAATCAGCGGTACTACCTGAATACGCTCCGCATC 777
Db      624 CTGNGNNGGCCNNNTNGTCNGNCGNCTCNGAGCTNCTNCATCGNACGNTNNGNATT 683
Qy      778 TATATCTCGAACAAGCTGAGCGGTCGGCGGTTGCTCGCTCATATACGCGCAAGATCTTC 837
Db      684 TWTATNCTCAACCGGCACATGCGGNGANTCAATGNGNCTCGTCTTCTNNGNANNTGCTC 743
Qy      838 TCAATCTCTCTGAGCTACGCACTCGGCGCATGCAAACTCAACATGTGTCATCTCCCTC 897
Db      744 TCGNTCTCTC-CGGGCTCGGTCGTCGTCGCGNCCNGNANGC--GNGTGTGTTTCTCACTA 800
Qy      898 AAGCTCAAGAACAGAAAGCTCCGCCCTTTCTCTCGAGGAGATCTGGGATGTGGCGGACATG 957
Db      801 AGNTNNAGTCGNNNCTGNCNNGTTCTCTCGNGGNGNNTCTGGGNGNTTNNNTNN 860
Qy      958 TCG 960
Db      861 CCG 863

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RESULT 7
BX463524/c
LOCUS   BX463524 Homo sapiens ADULT BRAIN Homo sapiens cDNA clone
DEFINITION
CS0DN003YI18 3-PRIME, mRNA sequence.
ACCESSION BX463524
VERSION   BX463524.2 GI:46502676
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Homiidae; Homo.
REFERENCE 1 (bases 1 to 1088)
          Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
          Full-length cDNA libraries and normalization
          Unpublished (2001)
COMMENT   On May 22, 2003 this sequence version replaced gi:31037372.
          Contact: Genoscope
          Genoscope - Centre National de Sequencage
          2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
          Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
          1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
          end enriched, double-strand cDNA was digested with Not I and cloned
          into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
          was not normalized. Library was constructed by Life Technologies, a
          division of Invitrogen.
          This sequence belongs to sequence cluster 9247.f
          For more information about this cluster, see
          http://www.genoscope.cns.fr/cdna?8=CS0DN003BE09NP1&c=9247.f.
          Location/Qualifiers
            1..1088
              /organism="Homo sapiens"
              /mol_type="mRNA"
              /db_xref="taxon:9606"
              /clone="CS0DN003YI18"
              /tissue_type="ADULT BRAIN"
              /dev_stage="adult"
              /clone_lib="Homo sapiens ADULT BRAIN"
              /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
              was primed with a NotI-oligo(dT) primer. Five prime end
              enriched, double-strand cDNA was digested with Not I and
              cloned into the Not I and EcoRV sites of the pCMVSPORT 6
              vector. Library was not normalized."

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FEATURES
  source
    Query Match          12.3%; Score 130; DB 5; Length 1088;
    Best Local Similarity 54.7%; Pred. No. 3.1e-24;
    Matches 321; Conservative 2; Mismatches 250; Indels 14; Gaps 3;

ORIGIN

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Qy      367 CCCTTCGCCGAGATCAGAGATGACTATCTCAOGTCAACCTTATCGTGGAGTTCCGC 426
Db      926 CGCTTTGCCCACTTCACGGRGCTGGCCATCATCTCACTCAGGAGATCGTGGACTCGCT 867
Qy      427 AAGGATTCGACGGTTGGCCAGATCTCGCAGCTGATCAATTTAGCTGCTTAAGGCT 486
Db      866 AAGCAAGTGGCTGCTTTCTTCGAGCTGGCGGAGGACAGATCGGCCCTCTCTCAAGGCA 807
Qy      487 TGCTCAAGTGAAGTAATGATGCTCCGAGTCCGCGACGATACGATGCGGCTCAGACAGT 546
Db      806 TCCACTATCGAGATCATGCTCTAGACAGACGACGAGCGCTACAAACAGAGAGAGTGT 747
Qy      547 GTTCTGTTCGCGAACAACAGAGGTACACTCGCGGACAACTACCGCAAGGCTGGCAT---G 603
Db      746 ATCACTCTTTGAAGGACTTCACTCCTACGCAAGGACGACTTCCACCGTGCAGGCTGCAG 687
Qy      604 GCCTACGCTCATCGAGGATCTACTGCACTTCTGCGGTCGATGTAATCTATGCGGCTTCGAC 663
Db      686 GTGGAGTTTCATCAACCCCATCTTCGAGTTCTTCGCGGCGCATGCGGCTGGGCTGGAC 627
Qy      664 AACATCCATTACGCGCTGCTCAGCGCTGTGCTCATCTTTT---CTGACCCGCCCAGGGTGT 720
Db      626 GACCTGAGTACGCCCTGCTCATCGCCATCAACATCTTCTCGGCCGACCGGCCCAACGTG 567
Qy      721 GAGCAGCGCAACTGTGTGGAAGAAATCCAGCGGTACTACCTGAATACGCTCCGCAATCTAT 780
Db      566 CAGGAGCGCGCGCGCTGTGAGGGGCTTTCAGCAGCCCTTACGTTGAGGCGCTGCTGCTCTAC 507
Qy      781 ATCTGAAACGAGCTGAGCGGCTCGGCGGTTGCTGCTCATATACGCAAGAGTCTCTCA 840
Db      506 ACGCGCATCAAGAGCGCGCAGGANNACGCTGCGC-----TTCGCGGATGCTCATG 455
Qy      841 ATCTCTCTGAGCTACGCACTCGGCTCGGATCAAAATCTCAACATGTGCTATCTCCCTCAAG 900
Db      454 AAGCTGTGAGCTTGCAGCGCTGAGCTGTGCTGCTGAGGAGGCTGCTCTCTCTCGCG 395
Qy      901 CTCAAGAACAGAAAGCTGCGGCTTTCTCTCAGGAGATCTGGGATGT 947
Db      394 CTCAGGACAAAGAGCTGCGGCTCTGCTGTCGAGATCTGGGACGT 348

RESULT 8
BX222200
LOCUS   BX222200
DEFINITION
AGENCOURT 7503312 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:6018964
5' mRNA sequence.
ACCESSION BX222200
VERSION   BX222200.1 GI:20403609
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Homiidae; Homo.
REFERENCE 1 (bases 1 to 867)
          NIH-MGC http://mgi.nci.nih.gov/.
          National Institutes of Health, Mammalian Gene Collection (MGC)
          Unpublished (1999)
          Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-remail.nih.gov
          Tissue Procurement: ATCC
          CDNA Library Preparation: Life Technologies, Inc.
          DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: L1AM13220 row: 1 column: 05
          High quality sequence stop: 674.
          Location/Qualifiers
            1..867
              /organism="Homo sapiens"

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REFERENCE		Hominidae; Homo.	
TITLE		1 (bases 1 to 1031)	
JOURNAL		NIH-MGC http://mgi.nci.nih.gov/.	
COMMENT		National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)	
		Contact: Robert Strausberg, Ph.D.	
		Email: cga@bbs-r@mail.nih.gov	
		Tissue Procurement: Lou Staudt	
		cDNA Library Preparation: Rubin Laboratory	
		DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)	
		Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:	
		http://image.llnl.gov	
		Plate: LLCW2067 row: k column: 11	
		High quality sequence stop: 634.	
FEATURES		Location/Qualifiers	
source		1..1031	
		/organism="Homo sapiens"	
		/mol_type="mRNA"	
		/db_xref="taxon:9606"	
		/clone="IMAGE:5814274"	
		/tissue_type="lymphoma, cell line"	
		/lab_host="DH10B (phage-resistant)"	
		/clone_lib="NIH_MGC_93"	
		/note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCCAGCAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."	
ORIGIN		Query Match 12.0%; Score 127; DB 3; Length 1031;	
		Best Local Similarity 54.0%; Pred. No. 2e-23;	
		Matches 322; Conservative 0; Mismatches 250; Indels 15; Gaps 3;	
QY	367	CCCTTCGGCAGATCAGAGATGACTATCTCCTCAGCGTCCAACTTATCGTGAGTTGCGG	426
Db	96	CGCTTTGCCCACTTCAGGAGCTGGCCATCATCTCAGTCCAGGAGATCGTGGACTTCGCT	155
QY	427	AAGGATTCAGAGTTGCGCAAGATCTCCAGCTGATCAAAATAGCTGCTTAAGGCT	486
Db	156	ARGCAAGTGCCTGGTTCCTGCACTGGCGCGGAGACAGATCGCCCTCTCTGAAGGCA	215
QY	487	TGCTCAAGTCAGGTAAATGATGCTCCGAGTCCGCGACGATACGATGCGGCTCAGACGT	546
Db	216	TCACATATCAGATATCTGCTTAGAGACAGCCAGGCGCTACAAACAGAGACAGATGT	275
QY	547	GTCTCTTCGCGAACAACCAAGCGTACATCTCGACAACTACCGCAAGCTGGCAT---	603
Db	276	ATCACCTTCTGAAGGACTTCACCTACAGCAAGACGACTTCACCGTGCAGGCTGCAG	335
QY	604	GCCTACGTCATCAGGATCTACTGCACTTCTGCGGTGATGTACTCTATGCGGTGGAC	663
Db	336	GTGGAGTTTCATCAACCCCATCTTCGAGTTCTCGCGGCGCATGCGGCGGCTGGGCT	395
QY	664	AACATCATTTACGGCTGCTCAGCGCTGTGTATCTTTT---CTGACCGCGCAGGTTG	720
Db	396	GACGTGATGATCGCTTCTATCGCCATCAACATCTTCGGCGGACCGGCCCAAGTG	455
QY	721	GAGCAGCGCAACTGTTGGAGAAATCCAGCGGTACTACCTGAATAGCTCCGCTCAT	780
Db	456	CAGAGCGCGCGCGTGGAGGCGTTGACAGCGCTTACGTGGAGGCGCTGCTGCTCTAC	515
QY	781	ATCTGAACAGCTGAGCGGTGCGCGGTGCTGCGTCTATATACGCAAGATCTCTCA	840
Db	516	ACGCGCATCAAGAGCGCGCAGACACGAC-----TGCGCTTCCGCGCATGCTCATG	566
QY	841	ATCTCTCTGAGCTACGACGCTCGGCATGCAAACTCCAACTGTGCATCTCCCTCAAG	900
Db	567	AAGCTGTGAGCTTGGCAAGCTGAGTCTGTGCACTCGAGCGAGTCTTGGCTTGGG	626
QY	901	CTCAAGAACAGAAAGCTGCGGCTTTCTCTGAGGAGATCTGGGATGTGGCGGACATGCG	960
Db	627	CTCAGGACAAAGAGCTGCGGCTCTGCTGTGGAGATCTGGGAGCTCCACGAGTGAAG	686
QY	961	CACACCCAAACGCGGCTCA 979	
Db	687	GGCTGGCCACCCAGCCCCA 705	
RESULT 9		1031 bp mRNA linear EST 29-MAR-2002	
LOCUS		BQ058428	
DEFINITION		AGENCOURT 6794704 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5814274	
		5', mRNA sequence.	
ACCESSION		BQ058428	
VERSION		BQ058428.1 GI:19817768	
KEYWORDS		EST.	
SOURCE		Homo sapiens (human)	
ORGANISM		Homo sapiens	
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
		Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	


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QY 781 ATCTGAAACAGCTGAGCGGTGGCGGTTCTCGCTCATATACGGCAAGATCTCTCA 840
Db 1452 ACAGGATCAAGCGCCACAGGACCAAGC-----TCGCTTCCACGCAATGCTCATG 1502
QY 841 ATCTCTCTGAGCTAGCAGCTCGGATGCAAAATCCAAATGTCATCTCCCTCAAG 900
Db 1503 AAGCTGGTGAAGCTGGGACCCCTCAGCTCGTGCATCGGAGCAGGTCTTTGATTCGA 1562
QY 901 CTCAGAACAGAAAGCTGGCGCTTCTTCGAGAGATCTGGGATGTGGCGGACATGTGC 960
Db 1563 CTCAGAGCAAGAAAGCTGGCGCTTCTTCGAGAGATCTGGGATGTGCACGAGTAGGGG 1622
QY 961 CACACCCCAACCGCGC 976
Db 1623 CAGCCAAAGTGCCCC 1638

RESULT 11
CN309352
LOCUS 1700599937470 GRN_PRRHEP Homo sapiens cDNA 5', mRNA linear EST 16-MAY-2004
DEFINITION CN309352
ACCESSION CN309352
VERSION 1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 651)
AUTHORS Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Pisk, G.J.,
Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,
Lebkowski, J. and Stanton, L.W.
TITLE Transcription characterization elucidates signaling networks that
control human ES cell growth and differentiation
JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
PUBMED 15146197
COMMENT Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
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FEATURES
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from DMSO-treated hES cell line H9 (p22) maintained in
feeder-free conditions"

ORIGIN
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Best Local Similarity 54.7%; Pred. No. 5e-23;
Matches 321; Conservative 0; Mismatches 251; Indels 15; Gaps 3;

QY 367 CCCTTCGCCGAGATCAGAGATGACTATCTCAGCGTCCAACTATTCGTGGAGTTCGCG 426
Db 74 CGCTTTGCCACTTACGGAGTGGCCATCATCTCAGTCAGGAGATCGTGGACTTCGCT 133
QY 427 AAGGGATTGGCGGTTGGCCAGATCTCGAGCCTGATCAATAGCTGCTTAAGGCT 486
Db 134 AAGCAATGTGCTGGTTTCTTCGAGCTGGCGGGAGACAGATCGCCCTCCTGAAGGCA 193
QY 487 TGCTCAAGTAGGTAATGATGCTCCGAGTGGCGGAGATACGATGGCGCTCAGACAGT 546

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Db 194 TCCATATCGAGATCATGCTGTCTAGAGACAGCCAGCGCTCAACACGAGACAGAGTGT 253
QY 547 GTTCTGTTTCGCAACAAACAGCGTACACTCCGCAACTACCGCAAGGCTGGCAT--G 603
Db 254 ATCACCTTCTTGAAGGACTTACCTACAGCAAGGACGACTTCCACCGTGCAGGCTGCAG 313
QY 604 GCCTAGGTCATCGAGGATCTACTGCACTTCTGCGGTGATGATCTCTATATGGTGGTGC 663
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QY 781 ATCTGTAAACAGCTGAGCGGTTGGCGGTTGTCGTCGTCATATAGGCAAGATCTCTCA 840
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QY 841 ATCTCTCTGAGCTACGCACTCGGCTCGGCAATGCAAACTCCAAATGTGCAATCTCCCTCAAG 900
Db 545 AAGCTGGTGAAGCTGGCGCTTCTTCGAGAGATCTGGGATGT 947
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LOCUS 1700599937470 GRN_PRRHEP Homo sapiens cDNA 5', mRNA linear EST 24-JUN-2003
DEFINITION CN309352
ACCESSION CN309352
VERSION 1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 667)
AUTHORS Wistow, G., Bernstein, S.L., Ray, S., Wyatt, M.K., Behal, A.,
Touchman, J.W., Bouffard, G., Smith, D. and Peterson, K.
TITLE Expressed sequence tag analysis of adult human iris for the NEIBank
Project: steroid-response factors and similarities with retinal
pigment epithelium
JOURNAL Mol. Vis. 8 (4), 185-195 (2002)
PUBMED 12107412
COMMENT Contact: Wistow G
Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
Email: graeme@helix.nih.gov
Plate: 19 row: g column: 05
Seq primer: M13RP1 reverse primer (ABI).
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library (bx) was normalized by self-subtraction. One

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portion of double stranded plasmid DNA representing the library was linearized by NotI. This NotI digested library was used as a template for biotinylated RNA synthesis using SP6 RNA polymerase. Another portion of the double stranded plasmid library was converted to single-stranded circles in vitro using Gene II and Exonuclease III (Life Technologies). Single-stranded DNA (1 mg) was hybridized (Cot 500) with 41 mg of Bio-RNA and vector blocking oligonucleotides. The hybridized Bio-RNA/ss-circles were removed by streptavidin:phenol extraction. EST analysis was performed on the library at the NIH Intramural Sequencing Center (NISC)."

ORIGIN

Query Match 11.9%; Score 125.4; DB 6; Length 667;
Best Local Similarity 54.7%; Pred. No. 5e-23;
Matches 321; Conservative 0; Mismatches 251; Indels 15; Gaps 3;

QY 367 CCCTTCGCCGATCAGAGATGACTATCTCAGGTCCCACTTATCGTGGATTGCG 426
DB 10 CGCTTTGCCCACTTCCAGGAGTGGCCATCATCTCAGTCCAGGAGATCGTGGACTTCGCT 69

QY 427 AAGGATTTGCCAGGTTTCGCCAAGATCTCGCAGCTGTATCAAAATTACGCTGCTTAAGGCT 486
DB 70 AAGCAAGTGCCTGTTTCTCGACCTGGCGGAGGACGATCGCCCTCTCGAAGCA 129

QY 487 TGCTCAAGTAGAGTAAATGATGCTCCGAGTCCGCGAGCATACGATGCGGCTCAGACAGT 546
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QY 547 GTTCTGTTCCGGAACAACAGCTGACTCTCGCAGCAACTACCGCAAGGCTGGAT---G 603
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QY 721 GAGCAGCGCAACTGTTGGAGAAATCCAGCGTACTCTGTAATACGCTTCGCAATCTAT 780
DB 370 CAGGAGCGGCGCGTGGAGCGTTGCGAGCAGCCCTACGTTGGAGGCGCTGCTGCTCTAC 429

QY 781 ATCTGTAACGAGTACGCGGTTCGCGGCTGCTGCTCATATACGCAAGATCTCTCA 840
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DB 481 AAGCTGTGAGCTTCGCGAGCTGAGCTCTGTGACTCGGAGCAGGTCTTCGCTTGGCG 540

QY 901 CTCAAGAACAGAAAGTTCGCGCTTCTCGTGGAGAGATCTGGGATGT 947
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RESULT 13

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DEFINITION AGENCOURT 7588981 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:6070455
5', mRNA sequence.

ACCESSION BQ214241
VERSION BQ214241.1 GI:20395641
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 918)

NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs@mail.nih.gov
Tissue Procurement: DCTD/DPG/Gazdar
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LLM13354 row: m column: 16
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Site: 2; SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.8 kb. Library constructed by Life
Technologies."

FEATURES
source

ORIGIN

Query Match 11.9%; Score 125.4; DB 3; Length 918;
Best Local Similarity 54.7%; Pred. No. 5.4e-23;
Matches 321; Conservative 0; Mismatches 251; Indels 15; Gaps 3;

QY 367 CCCTTCGCCGATCAGAGATGACTATCTCAGGTCCCACTTATCGTGGATTGCG 426
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QY 427 AAGGATTTGCCAGGTTTCGCCAAGATCTCGCAGCTGTATCAAAATTACGCTGCTTAAGGCT 486
DB 92 AAGCAAGTGCCTGTTTCTTCGAGCTGGCGCGGAGACAGATCGCCCTCTGAGGCA 151

QY 487 TGCTCAAGTAGAGTAAATGATGCTCCGAGTCCGCGAGCATACATGCGGCTCAGACAGT 546
DB 152 TCCACTATCGAGATCATGCTGTAGAGACAGCAGCGCGCTACAAACGACGACAGATGT 211

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QY 604 GCCTACGTCATCGAGGATCTACTGCACTTCTGCGGTGCAATGTACTCTATGGGTTGGAC 663
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DB 332 GACGCTGAGTACGCGCTGCTCATCGCATCAACATCTTCTCGCGCCGACCGGCCCAAGTG 391

QY 721 GAGCAGCGCAACTGTTGGAGAAATCCAGCGTACTACCTGAATACGCTCCGCTCAT 780
DB 392 CAGGAGCGGCGCGTGGAGGCTTTCAGACGCCCTACGAGGCGGCTGCTGCTCTAC 451

QY 781 ATCTTGAAACAGCTGAGCGGCTCGCGGCTTCTCGCTCATATACGCAAGATCTCTCA 840
DB 452 ACGGCATCAAGA-----GGCCGAGGACGAGCTGCGCTTCCCGCATGCTCATG 502

QY 841 ATCTCTCTGAGTACGAGCTCGGATGCAAACTCCAACTGTGATCTCCCTCAAG 900
DB 503 AAGCTGTGAGCTTCGCGAGCTGAGCTCTGTGACTCGGAGCAGGTCTTCGCTTGGCG 562

QY 901 CTCAAGAACAGAAAGTTCGCGCTTCTTCGAGGAGATCTGGGATGT 947
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Job time : 4084 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 31, 2006, 01:12:44 ; Search time 661 Seconds
(without alignments)

10627.210 Million cell updates/sec

Title: US-09-965-703A-3

Perfect score: 1054

Sequence: 1 cctgagtgctagtagaccga.....gtccggcgctgctctga 1054

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: Geneseqn1980s.*

2: Geneseqn1990s.*

3: Geneseqn2000s.*

4: Geneseqn2001as.*

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6: Geneseqn2002as.*

7: Geneseqn2002bs.*

8: Geneseqn2003as.*

9: Geneseqn2003bs.*

10: Geneseqn2003cs.*

11: Geneseqn2003ds.*

12: Geneseqn2004as.*

13: Geneseqn2004bs.*

14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1054	100.0	1054	6	ABs68150 DNA encod
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7	1054	100.0	1054	13	ABt08306 Ecr-based
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9	1054	100.0	1288	4	AAS15631 Spruce bu
10	1054	100.0	1288	6	ABs68144 DNA encod
11	1054	100.0	1288	6	ABt08298 Ecr-based
12	1029.4	97.7	1290	6	ABK49451 DNA encod
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14	1010.2	95.8	1073	6	ABK49461 DNA encod
15	1010.2	95.8	1073	9	ACf36064 C. fumife
16	1010.2	95.8	1073	12	ADH01013 Spruce bu
17	1010.2	95.8	1073	12	ADH00996 Spruce bu
18	1005	95.4	1110	4	AAS15632 Spruce bu
19	1005	95.4	1110	6	ABt08308 Ecr-based

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21	1005	95.4	1542	6	ABT08307	Abt08307 Ecr-based
22	1002	95.1	1623	6	ABs70117	ABs70117 Spruce bu
23	960	91.1	960	4	AAS15635	Aas15635 Spruce bu
24	960	91.1	960	6	ABs68117	ABs68117 DNA encod
25	960	91.1	960	6	ABT08278	ABt08278 Ecr-based
26	929	88.1	1247	4	AAS15666	Aas15666 Spruce bu
27	735	69.7	735	4	AAS15634	Aas15634 Spruce bu
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30	636.4	60.4	2126	3	AAJ10312	AaJ10312 European s
31	623.4	59.1	2840	6	ABT07274	ABt07274 Manduca s
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33	623.4	59.1	2840	12	ADT33132	Adt33132 Tobacco h
34	621.6	59.0	1500	6	ABT07331	ABt07331 Chimeric
35	621.6	59.0	1500	10	ADf49139	Adf49139 Ecdysone
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37	621.6	59.0	1767	10	ADF49192	Adf49192 Ecdysone
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40	617.2	58.6	1848	6	ABT07376	ABt07376 Chimeric
41	617.2	58.6	1848	10	ADF49206	Adf49206 Ecdysone
42	617	58.5	1518	6	ABT07344	ABt07344 Chimeric
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44	617	58.5	3972	6	ABT07353	ABt07353 Ecdysone
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ALIGNMENTS

RESULT 1

AAS15633

ID AAS15633 standard; DNA; 1054 BP.

XX

AC AAS15633;

XX

29-JAN-2002 (first entry)

XX

DE Spruce budworm Ecdysone receptor ligand binding domain CfEcrDEF DNA.

XX

KW Spruce budworm; Ecdysone receptor; Ecr; ligand binding domain; ds;

KW retinoid X receptor; RXR; DNA-binding domain; transactivation domain;

KW nuclear receptor; ultraspiracle; gene therapy; protein production;

KW antibody production; high throughput screening; HTS; transgenic plant;

KW transgenic animal; CfEcrDEF.

XX

OS Choristoneura fumiferana.

XX

FH Key

FT CDS

FT

FT

FT

FT

FT

FT

FT

FT

FT

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Location/Qualifiers

1. .1005

/tag= a

/product= "Ecr ligand binding domain"

/partial

/note= "No start codon"

WO200170816-A2.

27-SEP-2001.

21-MAR-2001; 2001WO-US009050.

22-MAR-2000; 2000US-0191355P.

20-FEB-2001; 2001US-0269799P.

(ROHM) ROHM & HAAS CO.

Palli SR, Kapitskaya MZ, Cress DE;

WPI; 2001-656841/75.

P-PSDB; AAU10257.

Ecdysone and retinoid X receptor based inducible gene expression systems

for use in e.g. gene therapy, large scale production of proteins and cell
-based high-throughput screening assays.

Claim 7; Page 90; 144pp; English.

The invention relates to Ecdysone and retinoid X receptor based inducible
gene expression systems useful for modulating gene expression in host
cells. The gene expression system encodes a polypeptide with a DNA-
binding domain recognizes a response element associated with a gene whose
expression is to be modulated and/or a ligand binding domain (LBD)
comprising a LBD from a nuclear receptor and a second gene expression
cassette capable of being expressed in a host cell comprising a
polynucleotide sequence encoding a second polypeptide comprising a trans-
activation domain and/or a LBD comprising a LBD from a nuclear receptor
other than ultraspiracle (USP) (the trans-activation domain is from a
nuclear receptor other than an ecdysone receptor, a retinoid X receptor
or a USP receptor and the LBDs from the first and second polypeptides are
different and dimerize). The ecdysone and retinoid X receptor based
inducible gene expression systems useful for modulating gene expression
in host cells, for use in gene therapy, large scale production of
proteins and antibodies, cell-based high-throughput screening assays
(HTS), functional genomic and regulation of traits in transgenic plants
and animals. The present sequence encodes a Spruce budworm Ecdysone
receptor ligand binding domain for use in an inducible gene expression
system of the invention

Sequence 1054 BP; 258 A; 318 C; 273 G; 205 T; 0 U; 0 Other;

Query Match	100.0%;	Score 1054;	DB 4;	Length 1054;
Best Local Similarity	100.0%;	Pred. No. 1.5e-281;		
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DB	61	AAGGAGAGACAAACCTGCTGTCAGCACACGAGGTGACGACCAATGCGGCCCATTT	120	
QY	121	ATGCAGTGTGAACCTCCACCTCTCTGAAGCAGCAGGATTCACGAAGTGTGCCAAGGTTT	180	
DB	121	ATGCAGTGTGAACCTCCACCTCTCTGAAGCAGCAGGATTCACGAAGTGTGCCAAGGTTT	180	
QY	181	CTCTCCGACAAAGCTGTTGGAGACAAACCGGAGAAAATCATCCCGATTGACAGCCAAC	240	
DB	181	CTCTCCGACAAAGCTGTTGGAGACAAACCGGAGAAAATCATCCCGATTGACAGCCAAC	240	
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DB	481	AAGGCTTGCTCAAGTGAAGTAAATGATGCTCCGAGTCCGCGGACGATGAGTGGGCTCA	540	
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QY	841	ATCTCTCTGAGTACGCAAGCTCGGCAATGCAAAATCCAAATGTCATCTCCCTCAAG	900	
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QY	901	CTCAAGAACAGAAAGCTGCGGCTTCTCTCGAGGAGATCTGGGATGCGGACATGTCG	960	
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DB	961	CACACCAACCGCGCTATCTCTGAGTCCCGCAGCAATCTCTAGCCCTGCGCGCACG	1020	
QY	1021	ATGCGCGATGCGCGCTCGGCGCGCTGCTCTGA	1054	
DB	1021	ATGCGCGATGCGCGCTCGGCGCGCTGCTCTGA	1054	
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AC	ABS68150;			
XX				
DT	18-NOV-2002 (first entry)			
XX				
DE	DNA encoding ecdysone receptor ligand binding domain #6.			
XX				
KW	Gene expression modulation system; DNA-binding domain; ecdysone receptor;			
KW	ligand binding domain; retinoid X receptor; RXR; transactivation domain;			
KW	gene therapy; large-scale production of protein; antibody production;			
XX	functional genomic; transgenic animal; ds.			
OS	Choristoneura fumiferana.			
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PN	WO200266614-A2.			
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PD	29-AUG-2002.			
XX				
PF	20-FEB-2002; 2002WO-US005706.			
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DR	WPI; 2002-674930/72.			
DR	P-PSDB; ABG92570.			
XX				
PT	Novel ecdysone receptor/chimeric retinoid X receptor-based inducible gene			
PT	expression system useful for modulating gene expression in a host cell			
PT	for gene therapy and large-scale production of proteins and antibodies.			
XX				
PS	Claim 4; Page 130; 140pp; English.			
XX				
CC	The invention describes a gene expression modulation system (I)			

comprising first and second gene expression cassettes that comprise polynucleotides encoding first and second hybrid polypeptides (P1,P2). P1 comprises a DNA-binding domain and an ecdysone receptor ligand binding domain or DNA-binding domain and a chimeric retinoid X receptor (RXR) ligand binding domain. P2 comprises a transactivation domain and RXR ligand binding domain or transactivation domain and ecdysone receptor ligand binding domain. (1) is useful for modulating the expression of a gene in a host cell, for applications such as gene therapy, large-scale production of proteins and antibodies, cell-based high throughput screening assays, functional genomics and regulation of traits in transgenic organisms. This sequence encodes an ecdysone receptor ligand binding domain useful in the creation of the gene expression modulation system

Query Match 100.0%; Score 1054; DB 6; Length 1054; Best Local Similarity 100.0%; Pred. No. 1.5e-281; Matches 1054; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGAGTGGTACCGAGACTCAGTGGCCCATGAGCGGAAAGAGAAAGCAAG 60
 DB 1 CCTGAGTGGTACCGAGACTCAGTGGCCCATGAGCGGAAAGAGAAAGCAAG 60
 QY 61 AAGGAGAGGACAACTGCTGTGACGACGAGCGGTGGACGACCATGCCGCCATT 120
 DB 61 AAGGAGAGGACAACTGCTGTGACGACGAGCGGTGGACGACCATGCCGCCATT 120
 QY 121 ATGCAAGTGTGAACCTCCACCTCTGAGCAGCAAGGATTCACGAAGTGTGCCAAGGTTT 180
 DB 121 ATGCAAGTGTGAACCTCCACCTCTGAGCAGCAAGGATTCACGAAGTGTGCCAAGGTTT 180
 QY 181 CTCTCCGACAAAGCTGTTGGAGACAAACCGGCGAGAAACATCCCCAGTTGACAGCCAAAC 240
 DB 181 CTCTCCGACAAAGCTGTTGGAGACAAACCGGCGAGAAACATCCCCAGTTGACAGCCAAAC 240
 QY 241 CAGCAGTCTCTATGCGCAGGCTCATCTGGTACGAGCGGTACGAGCGCTTCTGAT 300
 DB 241 CAGCAGTCTCTATGCGCAGGCTCATCTGGTACGAGCGGTACGAGCGCTTCTGAT 300
 QY 301 GAAGATTGAAGAGATTACGACAGTGGCGAGCAAGCGGACGATGAAGAGAGATCT 360
 DB 301 GAAGATTGAAGAGATTACGACAGTGGCGAGCAAGCGGACGATGAAGAGAGATCT 360
 QY 361 GACACTCCCTTCGCGCAGATCACAGAGATGACTATCTCAGCGTCCAACTTATCGTGGAG 420
 DB 361 GACACTCCCTTCGCGCAGATCACAGAGATGACTATCTCAGCGTCCAACTTATCGTGGAG 420
 QY 421 TTCCGGAAGGATTGCGAGGTTCCGAGATCTCGAGCGCTGATCAAAATACGCTGCTT 480
 DB 421 TTCCGGAAGGATTGCGAGGTTCCGAGATCTCGAGCGCTGATCAAAATACGCTGCTT 480
 QY 481 AAGCTTGTCTCAAGTGAAGTAAATGATCTCGAGTGGCGGACCATGATGCGGCTCA 540
 DB 481 AAGCTTGTCTCAAGTGAAGTAAATGATCTCGAGTGGCGGACCATGATGCGGCTCA 540
 QY 541 GACAGTGTCTGTGCGGACAAACCAAGCGTACACTCGCGCAACTACCGCAAGGCTGGC 600
 DB 541 GACAGTGTCTGTGCGGACAAACCAAGCGTACACTCGCGCAACTACCGCAAGGCTGGC 600
 QY 601 ATGCGCTACGTCATCGAGGATCTACTGCACTTTCGCGGTGCGATGATCTATGCGGTTG 660
 DB 601 ATGCGCTACGTCATCGAGGATCTACTGCACTTTCGCGGTGCGATGATCTATGCGGTTG 660
 QY 661 GACAACTCCATTACGCGCTGCTCAAGCTGTCTGATCTTTTCTGACCGGCGGAGTTG 720
 DB 661 GACAACTCCATTACGCGCTGCTCAAGCTGTCTGATCTTTTCTGACCGGCGGAGTTG 720
 QY 721 GAGCAGCGGCAACTGTGTGAGAAATCCAGCGGTACTACCTGAATAGCTCCGATCTAT 780
 DB 721 GAGCAGCGGCAACTGTGTGAGAAATCCAGCGGTACTACCTGAATAGCTCCGATCTAT 780
 QY 781 ATCTGAAACCAAGCTGAGCGGTCGGCGGTTCTGCTGCTATATACGGAAGATCTCTCA 840

781 ATCTGAAACAGCTGAGCGGTCGGCGGTTCTGCTCATATACGGAAGATCTCTCA 840
 QY 841 ATCTCTCTGAGCTACGACGCTCGGCATGCAAACTCCAACTGTGCTATCTCCCTCAAG 900
 DB 841 ATCTCTCTGAGCTACGACGCTCGGCATGCAAACTCCAACTGTGCTATCTCCCTCAAG 900
 QY 901 CTCAAGAACAGAAAGCTGCGGCTTTCTCTGAGGAGATCTGGGATGTGGCGGACATGTCG 960
 DB 901 CTCAAGAACAGAAAGCTGCGGCTTTCTCTGAGGAGATCTGGGATGTGGCGGACATGTCG 960
 QY 961 CACACCCCAACGCGGCTATCTCTGAGTCCCGGACCAATCTCTAGCCCCCTGCGGCGACG 1020
 DB 961 CACACCCCAACGCGGCTATCTCTGAGTCCCGGACCAATCTCTAGCCCCCTGCGGCGACG 1020
 QY 1021 ATGCGCGATGCGGCTCGGCGGCTGCTCTGA 1054
 DB 1021 ATGCGCGATGCGGCTCGGCGGCTGCTCTGA 1054

RESULT 3
 ABT08306
 ID ABT08306 standard; DNA; 1054 BP.
 XX AC ABT08306;
 XX DT 28-NOV-2002 (first entry)
 XX DE ECR-based inducible gene expression cassette related DNA SEQ ID No 53.
 XX KW Gene expression modulation system; large-scale production; gene therapy;
 XX KW Gene expression cassette; functional genomics; transgenic organism; ds.
 XX OS Choristoneura fumiferana.
 XX PN W0200266613-A2.
 XX PD 29-AUG-2002.
 XX PF 20-FEB-2002; 2002WO-US005235.
 XX PR 20-FEB-2001; 2001US-0269799P.
 XX PR 31-MAY-2001; 2001US-0294814P.
 XX PA (ROHM) ROHM & HAAS CO.
 XX PI Palli SR, Kapitskaya MZ;
 XX DR WPI; 2002-674929/72.
 XX PT Novel ecdysone receptor/invertebrate retinoid X receptor-based inducible
 PT gene expression system useful for modulating gene expression in host cell
 PT for gene therapy and large-scale production of proteins and antibodies.
 XX PS Claim 4; Page 116-117; 123pp; English.
 XX CC The invention relates to a novel gene expression modulation system
 CC comprising first and second gene expression cassettes that comprises
 CC polynucleotides encoding first and second hybrid polypeptides. The gene
 CC expression modulation system is useful for modulating the expression of a
 CC gene in a host cell comprising the gene to be modulated, for applications of a
 CC such as gene therapy, large-scale production of proteins and antibodies,
 CC cell-based high throughput screening assays, functional genomics and
 CC regulation of traits in transgenic organisms. This polynucleotide
 CC sequence represents DNA relating to the gene expression cassettes of the
 CC invention
 XX SQ Sequence 1054 BP; 258 A; 318 C; 273 G; 205 T; 0 U; 0 Other;

Query Match 100.0%; Score 1054; DB 6; Length 1054;
 Best Local Similarity 100.0%; Pred. No. 1.5e-281;
 Matches 1054; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGAGTGGCTAGTACCCGAGACTCAGTGGCCATGAAGCGGAAAGAGAAAGACACAG 60
 DB |||||
 QY 1 CCTGAGTGGCTAGTACCCGAGACTCAGTGGCCATGAAGCGGAAAGAGAAAGACACAG 60
 DB |||||
 QY 61 AAGGAGAGGACAAACTGCTGTGACGACGACGAGTGGACCAATGCCGCCATT 120
 DB |||||
 QY 61 AAGGAGAGGACAAACTGCTGTGACGACGACGAGTGGACCAATGCCGCCATT 120
 DB |||||
 QY 121 ATGCAAGTGAACCTCCACCTCTGAGGAGCAAGGATTCAGAGTGGTCCCAAGTTT 180
 DB |||||
 QY 121 ATGCAAGTGAACCTCCACCTCTGAGGAGCAAGGATTCAGAGTGGTCCCAAGTTT 180
 DB |||||
 QY 181 CTCTCCGACAACTGTTGGAGACAAACCGGACGAAACATCCCACTGGACAGCAAC 240
 DB |||||
 QY 181 CTCTCCGACAACTGTTGGAGACAAACCGGACGAAACATCCCACTGGACAGCAAC 240
 DB |||||
 QY 241 CAGCAGTTCCTTATCGCCAGGCTCATCTGTTACGAGCGGTACGAGCAGCCTTCTGAT 300
 DB |||||
 QY 241 CAGCAGTTCCTTATCGCCAGGCTCATCTGTTACGAGCGGTACGAGCAGCCTTCTGAT 300
 DB |||||
 QY 301 GAAGATTGAGAGGATTACGAGAGTGGCAGGAGCGGACGATGAAACGAGAGTCT 360
 DB |||||
 QY 301 GAAGATTGAGAGGATTACGAGAGTGGCAGGAGCGGACGATGAAACGAGAGTCT 360
 DB |||||
 QY 361 GACACTCCCTTCGCGCAGATCACAGAGATGACTATCTCAGCGTCCAACTTATCGTGGAG 420
 DB |||||
 QY 361 GACACTCCCTTCGCGCAGATCACAGAGATGACTATCTCAGCGTCCAACTTATCGTGGAG 420
 DB |||||
 QY 421 TTCCGAGAGGATTGCGCAGGTTGCGCAAGATCTCGCAGCCTGATCAAAATTACGCTGCTT 480
 DB |||||
 QY 421 TTCCGAGAGGATTGCGCAGGTTGCGCAAGATCTCGCAGCCTGATCAAAATTACGCTGCTT 480
 DB |||||
 QY 481 AAGCTTGTCTCAAGTGAAGTAAATGATGCTCGAGTGGCGGACGATGAGTGGGCTCA 540
 DB |||||
 QY 481 AAGCTTGTCTCAAGTGAAGTAAATGATGCTCGAGTGGCGGACGATGAGTGGGCTCA 540
 DB |||||
 QY 541 GACAGTGTCTGTTGCGGAAACCAAGCGTACACTCGCAGCAACTACCGCAAGGCTGGC 600
 DB |||||
 QY 541 GACAGTGTCTGTTGCGGAAACCAAGCGTACACTCGCAGCAACTACCGCAAGGCTGGC 600
 DB |||||
 QY 601 ATGSCCTACGCTACGAGGATCTACTGCACTTCTGCGGTCGATGATCTATGGCGTTG 660
 DB |||||
 QY 601 ATGSCCTACGCTACGAGGATCTACTGCACTTCTGCGGTCGATGATCTATGGCGTTG 660
 DB |||||
 QY 661 GACAGATTCATTAACGCGCTGCTCAGCGCTGTGTCATCTTTCTGACCGGCGAGGTTG 720
 DB |||||
 QY 661 GACAGATTCATTAACGCGCTGCTCAGCGCTGTGTCATCTTTCTGACCGGCGAGGTTG 720
 DB |||||
 QY 721 GAGCAGCGCAACTGTTGGAAGAAATCCAGCGGTACTCTGATATACGCTCCGCTAT 780
 DB |||||
 QY 721 GAGCAGCGCAACTGTTGGAAGAAATCCAGCGGTACTCTGATATACGCTCCGCTAT 780
 DB |||||
 QY 781 ATCTCTGAACAGCTGAGCGGTGCGCGCTGCTGCTGCTGCTATATACGCAAGATCTCTCA 840
 DB |||||
 QY 781 ATCTCTGAACAGCTGAGCGGTGCGCGCTGCTGCTGCTGCTATATACGCAAGATCTCTCA 840
 DB |||||
 QY 841 ATCTCTCTGAGCTACGCACTGCGGATGCAAACTCCAACTGTCATCTCTCTCAAG 900
 DB |||||
 QY 841 ATCTCTCTGAGCTACGCACTGCGGATGCAAACTCCAACTGTCATCTCTCTCAAG 900
 DB |||||
 QY 901 CTCAAGAACAGAAAGCTGCGCGCTTCTCTGAGGAGATCTGGGATGTCGCGGATGTCG 960
 DB |||||
 QY 901 CTCAAGAACAGAAAGCTGCGCGCTTCTCTGAGGAGATCTGGGATGTCGCGGATGTCG 960
 DB |||||
 QY 961 CACACCCAAACCGCGCTATCTCTGAGTCCCGCAGAACTCTAGACCGCTTCTGCGCAGC 1020
 DB |||||
 QY 961 CACACCCAAACCGCGCTATCTCTGAGTCCCGCAGAACTCTAGACCGCTTCTGCGCAGC 1020
 DB |||||
 QY 1021 ATGCGCGATGCGCGCTCGCGCGCTGCTCTGA 1054
 DB |||||
 QY 1021 ATGCGCGATGCGCGCTCGCGCGCTGCTCTGA 1054
 DB |||||

RESULT 4
 AAL49744
 ID AAL49744 standard; DNA; 1054 BP.
 XX
 AC AAL49744;
 XX
 DT 28-NOV-2002 (first entry)
 XX
 DE C fumiferana ecdysone receptor D,E,F domains coding sequence.
 XX
 KW Receptor; expression system; nuclear receptor; inducible gene expression;
 KW gene therapy; protein production; mutant; ecdysone receptor;
 KW retinoid X receptor; GAL4; LexA; VP16; B42; p65; gene; ds.
 XX
 OS Choristoneura fumiferana.
 XX
 WO200266615-A2.
 XX
 PD 29-AUG-2002.
 XX
 PF 20-FEB-2002; 2002WO-US005708.
 XX
 PR 20-FEB-2001; 2001US-0269799P.
 PR 21-AUG-2001; 2001US-0313908P.
 XX
 PA (ROHM) ROHM & HAAS CO.
 XX
 PI Palli SR, Kapitskaya MZ;
 XX
 WIPI; 2002-674931/72.
 XX
 PT Novel nuclear receptor polypeptides with substitution mutations, useful
 PT in gene expression modulation systems which are useful in gene therapy
 PT applications and cell-based high throughput screening assays.
 XX
 PS Example 1; Page 95; 110pp; English.
 XX
 CC The present invention relates to a gene expression modulation system
 CC containing a mutated coding sequence for a Group B nuclear receptor
 CC ligand. This is useful for modulating expression of a gene in a host
 CC cell, particularly in applications such as gene therapy, large scale
 CC production of proteins and antibodies, cell-based high throughput
 CC screening assays, functional genomics and regulation of traits in
 CC transgenic organisms. The present sequence is a coding sequence described
 CC in the exemplification of the invention
 XX
 SQ Sequence 1054 BP; 258 A; 318 C; 273 G; 205 T; 0 U; 0 Other;

Query Match 100.0%; Score 1054; DB 6; Length 1054;
 Best Local Similarity 100.0%; Pred. No. 1.5e-281;
 Matches 1054; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCTGAGTGGCTAGTACCCGAGACTCAGTGGCCATGAAGCGGAAAGAGAAAGACACAG 60
 DB |||||
 QY 1 CCTGAGTGGCTAGTACCCGAGACTCAGTGGCCATGAAGCGGAAAGAGAAAGACACAG 60
 DB |||||
 QY 61 AAGGAGAGGACAAACTGCTGTGACGACGAGCGGTGGACCAATGCCGCCATT 120
 DB |||||
 QY 61 AAGGAGAGGACAAACTGCTGTGACGACGAGCGGTGGACCAATGCCGCCATT 120
 DB |||||
 QY 121 ATGCAAGTGAACCTCCACCTCTGAGGAGCAAGGATTCAGAGTGGTCCCAAGTTT 180
 DB |||||
 QY 121 ATGCAAGTGAACCTCCACCTCTGAGGAGCAAGGATTCAGAGTGGTCCCAAGTTT 180
 DB |||||
 QY 181 CTCTCCGACAACTGTTGGAGACAAACCGGACGAAACATCCCACTGGACAGCAAC 240
 DB |||||
 QY 181 CTCTCCGACAACTGTTGGAGACAAACCGGACGAAACATCCCACTGGACAGCAAC 240
 DB |||||
 QY 241 CAGCAGTTCCTTATCGCCAGGCTCATCTGTTACGAGCGGTACGAGCAGCCTTCTGAT 300
 DB |||||
 QY 241 CAGCAGTTCCTTATCGCCAGGCTCATCTGTTACGAGCGGTACGAGCAGCCTTCTGAT 300
 DB |||||
 QY 301 GAAGATTGAGAGGATTACGAGAGTGGCAGGAGCGGACGATGAAACGAGAGTCT 360

Db 421 TTCCGGAAGGATTTCCAGGGTTCCGCAAGATCTCCGACCTGATCAAAATTACGCTGCTT 480
 Qy 481 AAGCTTGTCTCAAGTGAAGTAATGATGCTCCGAGTCCGCGACGATGAGTGGGCTCA 540
 Db 481 AAGGCTTGTCTCAAGTGAAGTAATGATGCTCCGAGTCCGCGACGATGAGTGGGCTCA 540
 Qy 541 GACAGTGTCTCTGTTCCGGAACCAACCAAGCGGTACACTCCGACCAACTACCGCAAGGCTGGC 600
 Db 541 GACAGTGTCTCTGTTCCGGAACCAACCAAGCGGTACACTCCGACCAACTACCGCAAGGCTGGC 600
 Qy 601 ATGGCCCTACGTCATCGAGGATCTACTGCACTTCTGCGGCTGTCATCTCTATGGGCTTG 660
 Db 601 ATGGCCCTACGTCATCGAGGATCTACTGCACTTCTGCGGCTGTCATCTCTATGGGCTTG 660
 Qy 661 GACACATCCATTAACGGCTGCTCAGGCTGTGTCATCTTTTCTGACCGGCCAGGGTTG 720
 Db 661 GACACATCCATTAACGGCTGCTCAGGCTGTGTCATCTTTTCTGACCGGCCAGGGTTG 720
 Qy 721 GAGCAGCGGCAACTGGTGGAGAAATCCAGCGGTACTACCTGAATACGCTCCGCACTAT 780
 Db 721 GAGCAGCGGCAACTGGTGGAGAAATCCAGCGGTACTACCTGAATACGCTCCGCACTAT 780
 Qy 781 ATCTGAAACAGCTGAGCGGTCGCGGCTGCGGCTGCTGCTGCTATATACGCGCAAGATCTCTCA 840
 Db 781 ATCTGAAACAGCTGAGCGGTCGCGGCTGCGGCTGCTGCTGCTATATACGCGCAAGATCTCTCA 840
 Qy 841 ATCTCTCTGAGTACGACGCTCGGATCGGATCGAAATCTCCAAATGTCATCTCCTCAAG 900
 Db 841 ATCTCTCTGAGTACGACGCTCGGATCGGATCGAAATCTCCAAATGTCATCTCCTCAAG 900
 Qy 901 CTCAAGAAAGAAAGCTGCGCGCTTTCTCTGAGGAGATCTGGATGTCGGGACATGTGCG 960
 Db 901 CTCAAGAAAGAAAGCTGCGCGCTTTCTCTGAGGAGATCTGGATGTCGGGACATGTGCG 960
 Qy 961 CACACCCAAACCGCGCTATCTCTGAGTCCCGCAGGAATCTCTAGCCCTCTGCGGCAAGC 1020
 Db 961 CACACCCAAACCGCGCTATCTCTGAGTCCCGCAGGAATCTCTAGCCCTCTGCGGCAAGC 1020
 Qy 1021 ATGCGCGATCGCGCTCGCGCGCTGCTCTGA 1054
 Db 1021 ATGCGCGATCGCGCTCGCGCGCTGCTCTGA 1054

RESULT 6
 ADR42608
 ID ADR42608 standard; DNA; 1054 BP.
 AC ADR42608;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Choristoneura fumiferana ecdysone receptor (EcR).
 XX
 KW spruce budworm; oxadiazoline ligand; gene expression modulation;
 KW gene expression cassette; ecdysone receptor complex; transgenic;
 KW genetic engineering; ecdysone receptor; EcR; gene; ds.
 XX
 OS Choristoneura fumiferana.
 XX
 PN US2004171651-A1.
 XX
 PD 02-SEP-2004.
 XX
 PF 19-FEB-2004; 2004US-00783810.
 XX
 PR 21-FEB-2003; 2003US-0449467P.
 XX
 PA (HORM/) HORMANN R E.
 PA (CHOR/) CHORTYK O.
 PA (LEDP/) LE D P.
 XX
 PI Hormann RE, Chortyk O, Le DP;

DR WPI; 2004-651695/63.
 XX New oxadiazoline ligands for regulating expression of nuclear receptor-based inducible genes in genetic engineering.
 PT Example 2; SEQ ID NO 1; 72pp; English.
 XX
 PS The invention describes oxadiazoline ligands. Also described are:
 CC modulating expression of a target gene in a host cell involving
 CC contacting the host cell with (I), the host cell includes first and
 CC second gene expression cassettes, or gene expression modulation system is
 CC introduced in the host cell; regulating endogenous or heterologous gene
 CC expression in a transgenic subject involving contacting (I) with an
 CC ecdysone receptor complex within the cells of the subject, the cells
 CC further contain a DNA binding sequence for the ecdysone receptor complex
 CC when in combination with the ligand, and formation of an ecdysone
 CC receptor complex-ligand DNA binding sequence complex induces expression
 CC of the gene; and producing a polypeptide involving selecting a cell which
 CC is insensitive to exposure to the ligand of formula (I), introducing into
 CC the cell a DNA construct and an ecdysone receptor complex, and exposing
 CC the cell to (I), the DNA construct comprises exogenous gene encoding the
 CC polypeptide, and a response element, the ecdysone receptor complex
 CC comprises DNA binding domain, a binding domain for the ligand, and
 CC transactivation domain. The ligands are useful for regulating expression
 CC of endogenous as well as heterologous genes in a transgenic subject (e.g.
 CC plant or mammal) during genetic engineering. The ligands provide an
 CC improved inducible gene expression system in both prokaryotic and
 CC eukaryotic host cells. This sequence represents Choristoneura fumiferana
 CC ecdysone receptor (EcR), used in the creation of a nuclear receptor-based
 CC inducible gene expression system.
 XX
 SQ Sequence 1054 BP; 258 A; 318 C; 273 G; 205 T; 0 U; 0 Other;

Query Match 100.0%; Score 1054; DB 13; Length 1054;
 Best Local Similarity 100.0%; Pred. No. 1.5e-281;
 Matches 1054; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CTGAGTGGTGTAGTACCCGAGACTCAGTGGCGCATGAGCGGAAAGAGAAAGCACAG 60
 Db 1 CTGAGTGGTGTAGTACCCGAGACTCAGTGGCGCATGAGCGGAAAGAGAAAGCACAG 60
 Qy 61 AAGGAGAAGGACAAACTGCTGTGACGACGAGCGTGGAGCAATCCGACCATCGCCCAT 120
 Db 61 AAGGAGAAGGACAAACTGCTGTGACGACGAGCGTGGAGCAATCCGACCATCGCCCAT 120
 Qy 121 ATGCACTGTGAACCTCCACCTCTCTGAAGCAGCAAGGATTCAGCAAGTGGTCCCAAGGTT 180
 Db 121 ATGCACTGTGAACCTCCACCTCTCTGAAGCAGCAAGGATTCAGCAAGTGGTCCCAAGGTT 180
 Qy 181 CTCTCCGACAGCTGTGGAGACAAACCGCGGAGAAAAATATCCCCAGTTGACAGCAAC 240
 Db 181 CTCTCCGACAGCTGTGGAGACAAACCGCGGAGAAAAATATCCCCAGTTGACAGCAAC 240
 Qy 241 CAGCAGTCTCTTATCCCGAGGCTCATCTGTGACGAGCGGTACGAGCAGCTTCGTAT 300
 Db 241 CAGCAGTCTCTTATCCCGAGGCTCATCTGTGACGAGCGGTACGAGCAGCTTCGTAT 300
 Qy 301 GAAGATTTGAAGAGGATTAACGACGAGCGTGGCAGCAAGCGGACGATCAAAACGAGAGTCT 360
 Db 301 GAAGATTTGAAGAGGATTAACGACGAGCGTGGCAGCAAGCGGACGATCAAAACGAGAGTCT 360
 Qy 361 GACATCTCCCTTCCCGCAGATCAAGAGATGATATCTCTCAAGTCCAACTATCTGAGGAG 420
 Db 361 GACATCTCCCTTCCCGCAGATCAAGAGATGATATCTCTCAAGTCCAACTATCTGAGGAG 420
 Qy 421 TTCCGGAAGGGATTGCGCAGGTTGCGCAAGATCTCCGAGCCTGATCAAAATTACGCTGCTT 480
 Db 421 TTCCGGAAGGGATTGCGCAGGTTGCGCAAGATCTCCGAGCCTGATCAAAATTACGCTGCTT 480
 Qy 481 AAGGCTTGTCTCAAGTGAAGGTAAATGATGCTCCGAGTCCGCGACGATACGATGCGGCTCA 540
 Db 481 AAGGCTTGTCTCAAGTGAAGGTAAATGATGCTCCGAGTCCGCGACGATACGATGCGGCTCA 540

Qy 541 GACAGTGTTCGTTCGGGACACCAAGCGTACACTCGCGCAAACTACCGCAAGGCTGGC 600
Db |||||
Qy 541 GACAGTGTTCGTTCGGGACACCAAGCGTACACTCGCGCAAACTACCGCAAGGCTGGC 600
Db |||||
Qy 601 ATGCGCTACGTCATCGAGGATCTACTGCACCTTCGCGGTGCAGTACTCTATGCGGTG 660
Db |||||
Qy 601 ATGCGCTACGTCATCGAGGATCTACTGCACCTTCGCGGTGCAGTACTCTATGCGGTG 660
Db |||||
Qy 661 GACAACATCCATTACGCGCTGCTCACGCGTGTGCTGCTATCTTTCTGACCGGCCAGGGTTG 720
Db |||||
Qy 721 GAGCAGCGCAACTGCTGGAAGAAATCAGCGGTACTACCTGAATAGCTCCGCACTAT 780
Db |||||
Qy 721 GAGCAGCGCAACTGCTGGAAGAAATCAGCGGTACTACCTGAATAGCTCCGCACTAT 780
Db |||||
Qy 781 ATCTCTGAACAGCTGAGCGGTGCGCGGTTCGTCGCTCATATACGCGCAAGTCTCTCA 840
Db |||||
Qy 781 ATCTCTGAACAGCTGAGCGGTGCGCGGTTCGTCGCTCATATACGCGCAAGTCTCTCA 840
Db |||||
Qy 841 ATCTCTCTGAGCTACGCAAGCTCGGCATGCGCAATCCAACTCCCAATGTCATCTCCCTCAAG 900
Db |||||
Qy 841 ATCTCTCTGAGCTACGCAAGCTCGGCATGCGCAATCCAACTCCCAATGTCATCTCCCTCAAG 900
Db |||||
Qy 901 CTGAAGAACAGAAAGCTGCGGCTTTCTCGAGGAGATCTGGGATGCGCGAATGTGCG 960
Db |||||
Qy 901 CTGAAGAACAGAAAGCTGCGGCTTTCTCGAGGAGATCTGGGATGCGCGAATGTGCG 960
Db |||||
Qy 961 CACACCCACCGCGGCTATCTCGAGTCCCGGCTGCTCTGA 1054
Db |||||
Qy 961 CACACCCACCGCGGCTATCTCGAGTCCCGGCTGCTCTGA 1054
Db |||||

RESULT 7

ADRS57970

ID ADRS57970 standard; DNA; 1054 BP.

XX

AC ADRS57970;

XX

DT 18-NOV-2004 (first entry)

XX

XX Choristoneura fumiferana EcR gene regulated by diacylhydrazine ligand.

XX

KW ds; cytostatic; gene therapy; diacylhydrazine ligand;

KW gene expression modulation; ecdysone receptor; functional genomics;

KW proteomics; metabolomics; transgenic organism; cancer therapy;

KW genetic disorder.

XX

XX Choristoneura fumiferana.

XX

PN W02004072254-A2.

XX

XX 26-AUG-2004.

XX

XX 10-FEB-2004; 2004WO-US003775.

XX

XX 10-FEB-2003; 2003US-0446233P.

XX

XX 09-FEB-2004; 2004US-00775883.

XX

XX (NEW-) NEW RHEOGENE LLC.

XX

XX Hormann RE, Tice CM, Chortyk O, Smith H, Meteyer T;

XX

XX WPI; 2004-642299/62.

XX

XX Novel diacylhydrazine ligands, useful for modulating expression of

XX exogenous genes in plants or mammals through ecdysone receptor complex.

XX

XX Example 2; SEQ ID NO 1; 120pp; English.

XX

PS

XX

CC The invention relates to novel diacylhydrazine ligands (I). (I) is useful
CC for modulating expression of target gene in host cell, modulating or
CC expression of one or more exogenous genes, regulating endogenous or
CC heterologous gene expression in transgenic subject by contacting (I) with
CC ecdysone receptor complex within cells of subject, where formation of
CC ecdysone receptor complex-(I)-DNA binding sequence complex induces
CC expression of gene. (I) is useful in gene therapy, large scale production
CC of proteins and antibodies, cell-based high throughput screening assays,
CC functional genomics, proteomics, metabolomics, and regulation of traits
CC in transgenic organism, where control of gene expression is desired and
CC for modulating the expression of genes that encode biologically active
CC proteins of interest, such as secondary proteins, genes that encode e.g.
CC blood clotting factors, hormones, enzymes, inhibitor substances and genes
CC useful in cancer therapy and treatment of genetic disorders. (I) is non-
CC steroidal ligand useful in nuclear receptor-based inducible gene
CC expression system. (I) is effective in controlling gene expression and
CC enables regulation of metabolism and to tailor expression levels to suit
CC the users requirements. This sequence represents an example of a gene
CC regulated by the compounds of the invention.

XX

SQ Sequence 1054 BP; 258 A; 318 C; 273 G; 205 T; 0 U; 0 Other;

Query Match 100.0%; Score 1054; DB 13; Length 1054;
Best Local Similarity 100.0%; Pred. No. 1.5e-281;
Matches 1054; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTGAGTGGCTAGTACCCGAGACTCAGTGGCCATGAAGCGGAAGAGAAAGCAAGCAAG 60
Db |||||

Qy 1 CCTGAGTGGCTAGTACCCGAGACTCAGTGGCCATGAAGCGGAAGAGAAAGCAAGCAAG 60
Db |||||

Qy 61 AAGGAGAAGGACAAATGCTGTGACGACGACGCGTGGACGACCATGCGGCCCATTT 120
Db |||||

Qy 61 AAGGAGAAGGACAAATGCTGTGACGACGACGCGTGGACGACCATGCGGCCCATTT 120
Db |||||

Qy 121 ATGCAAGTGAACCTCCACCTCTCTGAGCAGCAAGGATTCACGAAGTGGTCCCAAGGTTT 180
Db |||||

Qy 121 ATGCAAGTGAACCTCCACCTCTCTGAGCAGCAAGGATTCACGAAGTGGTCCCAAGGTTT 180
Db |||||

Qy 181 CTCTCGACAAAGCTGTTGGAGACAAACCGGCAGAAAACATCCCGAGTTGACAGCCCAAC 240
Db |||||

Qy 181 CTCTCGACAAAGCTGTTGGAGACAAACCGGCAGAAAACATCCCGAGTTGACAGCCCAAC 240
Db |||||

Qy 241 CAGCAGTTCCTTATCGCCAGGCTCATCTGTGTACAGGACGGGTACGAGCAGCCTTCTGAT 300
Db |||||

Qy 241 CAGCAGTTCCTTATCGCCAGGCTCATCTGTGTACAGGACGGGTACGAGCAGCCTTCTGAT 300
Db |||||

Qy 301 GAAGATTGAAGAGATTACGCGAGCTGCGCAGCAAGCGGACGATGAAACGAAAGATCT 360
Db |||||

Qy 301 GAAGATTGAAGAGATTACGCGAGCTGCGCAGCAAGCGGACGATGAAACGAAAGATCT 360
Db |||||

Qy 361 GACACTCCCTTCGCGCAGATCAGAGATGACTATCTCAGCGTCCAACTTATCGTGGAG 420
Db |||||

Qy 361 GACACTCCCTTCGCGCAGATCAGAGATGACTATCTCAGCGTCCAACTTATCGTGGAG 420
Db |||||

Qy 421 TTGCGAAGGATTCGCGAGGTTTCGCGAGGTTTCGCGAGGTTTCGCGAGGTTTCGCGAGG 480
Db |||||

Qy 421 TTGCGAAGGATTCGCGAGGTTTCGCGAGGTTTCGCGAGGTTTCGCGAGGTTTCGCGAGG 480
Db |||||

Qy 481 AAGGCTTGTCAAGTGAAGGTAATGATGCTCCGAGTCCGCGACGATACGATGCGGCTCA 540
Db |||||

Qy 481 AAGGCTTGTCAAGTGAAGGTAATGATGCTCCGAGTCCGCGACGATACGATGCGGCTCA 540
Db |||||

Qy 541 GACAGTGTTCGTTCGCGAACCAAGCGTACACTCGCGACAACTACCGCAAGGCTGGC 600
Db |||||

Qy 541 GACAGTGTTCGTTCGCGAACCAAGCGTACACTCGCGACAACTACCGCAAGGCTGGC 600
Db |||||

Qy 601 ATGCGCTTACCTCATCGAGGATCTACTGCACTTCTGCGGTCGATGCTACTCTATGGCGTTG 660
Db |||||

Qy 601 ATGCGCTTACCTCATCGAGGATCTACTGCACTTCTGCGGTCGATGCTACTCTATGGCGTTG 660
Db |||||

Qy 661 GACAACATCCATTACGCGCTGCTCACGCGTGTGCTGCTATCTTTCTGACCGGCCAGGGTTG 720
Db |||||

QY 781 ATCTGTAACGAGCTGAGCGGTTCGGCGTTCGCTCATATATACGCGAAGATCTCTCA 840
Db 781 ATCTGTAACGAGCTGAGCGGTTCGGCGTTCGCTCATATATACGCGAAGATCTCTCA 840
QY 841 ATCTCTCTGAGCTACGACGCTCGGATGCAAACTCCAACTGTCATCTCCCTCAAG 900
Db 841 ATCTCTCTGAGCTACGACGCTCGGATGCAAACTCCAACTGTCATCTCCCTCAAG 900
QY 901 CTCAAGAACAGAAAGCTGCGCCCTTTCTCGAGGAGATCTGGGATGTGGCGGACATGTGC 960
Db 901 CTCAAGAACAGAAAGCTGCGCCCTTTCTCGAGGAGATCTGGGATGTGGCGGACATGTGC 960
QY 961 CAGACCCACCGCGCTATCTCTGAGTCCCGGACGATCTCTAGCCCTCGCGGACGC 1020
Db 961 CAGACCCACCGCGCTATCTCTGAGTCCCGGACGATCTCTAGCCCTCGCGGACGC 1020
QY 1021 ATCCCGATGCGCGTTCGGCGGCTGCTCTGA 1054
Db 1021 ATCCCGATGCGCGTTCGGCGGCTGCTCTGA 1054

RESULT 9

AAS15631
ID AAS15631 standard; DNA; 1288 BP.

AC AAS15631;

XX 29-JAN-2002 (first entry)

XX Spruce budworm Ecdysone receptor ligand binding domain CfEcrRDEP DNA.

XX Spruce budworm; Ecdysone receptor; EcR; ligand binding domain; ds;
KW retinoid X receptor; RXR; DNA-binding domain; transactivation domain;
KW nuclear receptor; ultraspiracle; gene therapy; protein production;
KW antibody production; high throughput screening; HTS; transgenic plant;
KW transgenic animal; CfEcrRDEP.

XX Choristoneura fumiferana.

XX Key Location/Qualifiers

PH 1. 1239
FT CDS
FT /*tag= a
FT /product= "EcR ligand binding domain"
FT /partial
FT /note= "No start codon"

XX W0200170816-A2.

XX 27-SEP-2001.

XX 21-MAR-2001; 2001WO-US009050.

XX 22-MAR-2000; 2000US-0191355P.

XX 20-FEB-2001; 2001US-0269799P.

XX (ROHM) ROHM & HAAS CO.

XX Palli SR, Kapiteckaya MZ, Cress DE;

XX WPI; 2001-656841/75.

XX P-PSDB; AAU10255.

XX Ecdysone and retinoid X receptor based inducible gene expression systems
PT for use in e.g. gene therapy, large scale production of proteins and cell
PT -based high-throughput screening assays.

XX Claim 7; Page 88-89; 144pp; English.

XX The invention relates to Ecdysone and retinoid X receptor based inducible
CC gene expression systems useful for modulating gene expression in host
CC cells. The gene expression system encodes a polypeptide with a DNA-
CC binding domain recognizes a response element associated with a gene whose
CC expression is to be modulated and/or a ligand binding domain (LBD)

CC comprising a LBD from a nuclear receptor and a second gene expression
CC cassette capable of being expressed in a host cell comprising a
CC polynucleotide sequence encoding a second polypeptide comprising a trans-
CC activation domain and/or a LBD comprising a LBD from a nuclear receptor
CC other than ultraspiracle (USP) (the trans-activation domain is from a
CC nuclear receptor other than an ecdysone receptor, a retinoid X receptor
CC or a USP receptor and the LBDs from the first and second polypeptides are
CC different and dimerize). The ecdysone and retinoid X receptor based
CC inducible gene expression systems useful for modulating gene expression
CC in host cells, for use in gene therapy, large scale production of
CC proteins and antibodies, cell-based high-throughput screening assays
CC (HTS), functional genomic and regulation of traits in transgenic plants
CC and animals. The present sequence encodes a Spruce budworm Ecdysone
CC receptor ligand binding domain for use in an inducible gene expression
CC system of the invention

XX SQ Sequence 1288 BP; 318 A; 368 C; 346 G; 256 T; 0 U; 0 Other;

Query Match 100.0%; Score 1054; DB 4; Length 1288;

Best Local Similarity 100.0%; Pred. No. 1.6e-281;

Matches 1054; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGAGTGCCTAGTACCCGAGACTCAGTGCCTCATGAAGCGGAAAGAAAGACACAG 60
Db 235 CCTGAGTGCCTAGTACCCGAGACTCAGTGCCTCATGAAGCGGAAAGAAAGACACAG 294
QY 61 AAGGAGAAAGACAAACTGCTGTGACGACGCGTGGACACCAATGCCGCCCATT 120
Db 295 AAGGAGAAAGACAAACTGCTGTGACGACGCGTGGACACCAATGCCGCCCATT 354
QY 121 ATGCAAGTGAACCTCCACTCTGTAAGCAGAGAGATTCAGAAAGTGGTCCCAAGGTTT 180
Db 355 ATGCAAGTGAACCTCCACTCTGTAAGCAGAGAGATTCAGAAAGTGGTCCCAAGGTTT 414
QY 181 CTCTCCGACAAAGCTGTTGGAGACAAACCCGCGAGAAACATCCCCAGTGGACAGCCAAC 240
Db 415 CTCTCCGACAAAGCTGTTGGAGACAAACCCGCGAGAAACATCCCCAGTGGACAGCCAAC 474
QY 241 CAGCAGTTCCTTATCGCCAGGCTCATCTGTGTACGAGCGGTACGAGCAGCCTTCTGAT 300
Db 475 CAGCAGTTCCTTATCGCCAGGCTCATCTGTGTACGAGCGGTACGAGCAGCCTTCTGAT 534
QY 301 GAGATTTGAAGAGGATTCGCGAGAGCTGGCGAGCAAGCGGAGATGAAAGAGTCT 360
Db 535 GAGATTTGAAGAGGATTCGCGAGAGCTGGCGAGCAAGCGGAGATGAAAGAGTCT 594
QY 361 GACACTCCCTTCGCGCAGATCAGAGATGACTATCTCTCGGTCCCACTTATCGTGGAG 420
Db 595 GACACTCCCTTCGCGCAGATCAGAGATGACTATCTCTCGGTCCCACTTATCGTGGAG 654
QY 421 TTGCGAAGGAGATTGCGCAGGTTTCGCAAGATCTCGCAGCTCATCAAAATTACGCTGCTT 480
Db 655 TTGCGAAGGAGATTGCGCAGGTTTCGCAAGATCTCGCAGCTCATCAAAATTACGCTGCTT 714
QY 481 AAGGCTTGCTCAAGTGAAGTAAATGATGCTCCGAGTCCGCGAGATACGATGCGGCTCA 540
Db 715 AAGGCTTGCTCAAGTGAAGTAAATGATGCTCCGAGTCCGCGAGATACGATGCGGCTCA 774
QY 541 GACAGTGTCTCTGTTCCGGAACCAAGCGGTACTCTCGCGCAACTACCCGAGGCTGGC 600
Db 775 GACAGTGTCTCTGTTCCGGAACCAAGCGGTACTCTCGCGCAACTACCCGAGGCTGGC 834
QY 601 ATGCGCTTACGCTACGAGGATCTACTGCACTTCTGCGGCTGATGATCTATGCGGCTTG 660
Db 835 ATGCGCTTACGCTACGAGGATCTACTGCACTTCTGCGGCTGATGATCTATGCGGCTTG 894
QY 661 GACAACATCCATTACGCGTGTCTCAGCGTGTGCTCATCTTTTGTGACCGCGCAGGCTTG 720
Db 895 GACAACATCCATTACGCGTGTCTCAGCGTGTGCTCATCTTTTGTGACCGCGCAGGCTTG 954
QY 721 GAGCAGCGCACTGTGTGGAGAAATTCAGCGGTACTACTGTGATAGCTCCGCACTAT 780
Db 955 GAGCAGCGCACTGTGTGGAGAAATTCAGCGGTACTACTGTGATAGCTCCGCACTAT 1014

QY 781 ATCTCTGAGCTGAGCGGTGGCGGTTCTGTCGTCATATACGGCAGATCTCTCA 840
 Db 1015 ATCTCTGAGCAGCTGAGCGGTGGCGGTTCTGTCGTCATATACGGCAGATCTCTCA 1074
 QY 841 ATCTCTCTGAGCTGAGCGGTGGCGGTCGTCATATACGGCAGATCTCTCAAG 900
 Db 1075 ATCTCTCTGAGCTGAGCGGTGGCGGTCGTCATATACGGCAGATCTCTCAAG 1134
 QY 901 CTCAAGAACAGAAAGCTGCGGCTTTCTCTGAGGAGATCTGGGATGTCGCGGACATGTCG 960
 Db 1135 CTCAAGAACAGAAAGCTGCGGCTTTCTCTGAGGAGATCTGGGATGTCGCGGACATGTCG 1194
 QY 961 CACACCCACCGCGGCTATCTCTGAGTCCCGCCACGAATCTTAGCCCTGCGCGCACGC 1020
 Db 1195 CACACCCACCGCGGCTATCTCTGAGTCCCGCCACGAATCTTAGCCCTGCGCGCACGC 1254
 QY 1021 ATCGCGATGCGCGGTCCGCGGCTGCTCTGA 1054
 Db 1255 ATCGCGATGCGCGGTCCGCGGCTGCTCTGA 1288

RESULT 10

ID ABS68144 standard; DNA; 1288 BP.
 AC ABS68144;

XX 18-NOV-2002 (first entry)

XX DNA encoding ecdysone receptor ligand binding domain #5.
 XX Gene expression modulation system; DNA-binding domain; ecdysone receptor;
 KW ligand binding domain; retinoid X receptor; RXR; transactivation domain;
 KW gene therapy; large-scale production of protein; antibody production;
 KW functional genomic; transgenic animal; ds.
 XX Choristoneura fumiferana.
 XX WO20026614-A2.
 XX 29-AUG-2002.
 XX 20-FEB-2002; 2002WO-US005706.
 XX 20-FEB-2001; 2001US-0269799P.
 PR 31-MAY-2001; 2001US-0294814P.
 PR 31-MAY-2001; 2001US-0294819P.
 XX (ROHM) ROHM & HAAS CO.
 PA Palli SR, Kapitskaya MZ;
 PI WPI; 2002-674930/72.
 DR P-PSDB; ABG92569.
 DR Novel ecdysone receptor/chimeric retinoid X receptor-based inducible gene
 PT expression system useful for modulating gene expression in a host cell
 PT for gene therapy and large-scale production of proteins and antibodies.
 XX Claim 4; Page 127-128; 140pp; English.
 XX The invention describes a gene expression modulation system (I)
 CC comprising first and second gene expression cassettes that comprise
 CC polynucleotides encoding first and second hybrid polypeptides (P1,P2). P1
 CC comprises a DNA-binding domain and an ecdysone receptor ligand binding
 CC domain or DNA-binding domain and a chimeric retinoid X receptor (RXR)
 CC ligand binding domain. P2 comprises a transactivation domain and RXR
 CC ligand binding domain or transactivation domain and ecdysone receptor
 CC ligand binding domain. (I) is useful for modulating the expression of a
 CC gene in a host cell, for applications such as gene therapy, large-scale
 CC production of proteins and antibodies, cell-based high throughput
 CC screening assays, functional genomics and regulation of traits in

CC transgenic organisms. This sequence encodes an ecdysone receptor ligand
 CC binding domain useful in the creation of the gene expression modulation
 CC system
 XX Sequence 1288 BP; 318 A; 368 C; 346 G; 256 T; 0 U; 0 Other;
 Query Match 100.0%; Score 1054; DB 6; Length 1288;
 Best Local Similarity 100.0%; Pred. No. 1.6e-281;
 Matches 1054; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTGTAGTGTGATGATCCGAGACTCAGTGGCCATGAGCGGAAAGAGAAAGACACAG 60
 Db 235 CTGTAGTGTGATGATCCGAGACTCAGTGGCCATGAGCGGAAAGAGAAAGACACAG 294
 QY 61 AAGGAGAGGACAAATCTGCTGTTCAGACGACGAGCGGTGGACCAATGCGGCCCAT 120
 Db 295 AAGGAGAGGACAAATCTGCTGTTCAGACGACGAGCGGTGGACCAATGCGGCCCAT 354
 QY 121 ATGCAAGTGTGAACCTCCAGCTCTGAGCAGCAGGATTTACGAGTGGTCCCAAGGTTT 180
 Db 355 ATGCAAGTGTGAACCTCCAGCTCTGAGCAGCAGGATTTACGAGTGGTCCCAAGGTTT 414
 QY 181 CTCTCCGACAAAGCTGTGTGGAGACAAACCGGACAGAAAAACATCCCCCAGTTGACAGCAAC 240
 Db 415 CTCTCCGACAAAGCTGTGTGGAGACAAACCGGACAGAAAAACATCCCCCAGTTGACAGCAAC 474
 QY 241 CAGCAGTTCTTATGCGCAGGCTCATCTGTTACAGGACGCGGTACGAGCAGCCTTCAT 300
 Db 475 CAGCAGTTCTTATGCGCAGGCTCATCTGTTACAGGACGCGGTACGAGCAGCCTTCAT 534
 QY 301 GAAGATTTGAAGAGGATTTAGCAGAGCTGGCAGCAGCGGACGATGAAACGAGAGTCT 360
 Db 535 GAAGATTTGAAGAGGATTTAGCAGAGCTGGCAGCAGCGGACGATGAAACGAGAGTCT 594
 QY 361 GACATCTCCCTTCGCGCAGATTCAGAGATGACTATCTCAGCGTCAACTTATCTGCGGAG 420
 Db 595 GACATCTCCCTTCGCGCAGATTCAGAGATGACTATCTCAGCGTCAACTTATCTGCGGAG 554
 QY 421 TTCGGAAGGAGTTGCGCAGGTTTGGCAAGATCTTCGACGCTGATCAAAATAGCTGCTT 480
 Db 655 TTCGGAAGGAGTTGCGCAGGTTTGGCAAGATCTTCGACGCTGATCAAAATAGCTGCTT 714
 QY 481 AAGGCTTGTCTAAGTGAAGTGAATGATGCTCGAGTCCGCGGACGATACGATGGGCTCA 540
 Db 715 AAGGCTTGTCTAAGTGAAGTGAATGATGCTCGAGTCCGCGGACGATACGATGGGCTCA 774
 QY 541 GACAGTGTCTGTTCGCGAACAACCAAGCGTACACTCGGACAACTACCGCAAGGCTGGC 600
 Db 775 GACAGTGTCTGTTCGCGAACAACCAAGCGTACACTCGGACAACTACCGCAAGGCTGGC 834
 QY 601 ATGGCTTACGTATCAGGATCTATGCACTTTCGCGGTGCAATGATCTATGGCGTTG 660
 Db 835 ATGGCTTACGTATCAGGATCTATGCACTTTCGCGGTGCAATGATCTATGGCGTTG 894
 QY 661 GACAAATCATTACCGCTGCTCAGCGTGTGCTCATCTTTTCTGACCGGCGAGGTTG 720
 Db 895 GACAAATCATTACCGCTGCTCAGCGTGTGCTCATCTTTTCTGACCGGCGAGGTTG 954
 QY 721 GACGACGCGCAACTGGTGGAGAAATTCAGCGGTACTTACTGAAATACGCTCCGATCTAT 780
 Db 955 GACGACGCGCAACTGGTGGAGAAATTCAGCGGTACTTACTGAAATACGCTCCGATCTAT 1014
 QY 781 ATCTGAAACAGCTGAGCGGTTGCGCGGTTTCTGCGTCAATATACGGCAGATCTCTCA 840
 Db 1015 ATCTGAAACAGCTGAGCGGTTGCGCGGTTTCTGCGTCAATATACGGCAGATCTCTCA 1074
 QY 841 ATCTCTCTGAGCTAGCAGCTCGGCGATGCAAAATCCCAAGTGTGATCTCTCTCAAG 900
 Db 1075 ATCTCTCTGAGCTAGCAGCTCGGCGATGCAAAATCCCAAGTGTGATCTCTCTCAAG 1134
 QY 901 CTCAAGAACAGAAAGCTGCGGCTTTCTCTGAGGAGATCTGGGATGTCGCGGACATGTCG 960
 Db 1135 CTCAAGAACAGAAAGCTGCGGCTTTCTCTGAGGAGATCTGGGATGTCGCGGACATGTCG 1194

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QY 961 CACACCCAAACCGCGCTATCTCGAGTCCCCCAACGAATCTTAGCCCTCGCGCAGC 1020
Db 1195 CACACCCAAACCGCGCTATCTCGAGTCCCCCAACGAATCTTAGCCCTCGCGCAGC 1254
QY 1021 ATGCCGATCGCGGTCGGCCGGCTGCTCTGA 1054
Db 1255 ATGCCGATCGCGGTCGGCCGGCTGCTCTGA 1288

RESULT 11
ABT08298
ID ABT08298 standard; DNA; 1288 BP.
XX
AC AC
XX
DT 28-NOV-2002 (first entry)
XX
DE BCR-based inducible gene expression cassette related DNA SEQ ID No 45.
KW Gene expression modulation system; large-scale production; gene therapy;
KW gene expression cassette; functional genomics; transgenic organism; ds.
XX
XX Choriostoneura fumiferana.
XX
PN WO200266613-A2.
XX
PD 29-AUG-2002.
XX
PF 20-FEB-2002; 2002WO-US005235.
XX
PR 20-FEB-2001; 2001US-0269799P.
XX
PR 31-MAY-2001; 2001US-0294814P.
XX
PA (ROHM ) ROHM & HAAS CO.
XX
PI Palli SR, Kapitskaya MZ;
XX
XX WPI; 2002-674929/72.
XX
PT Novel ecdysone receptor/invertebrate retinoid X receptor-based inducible
PT gene expression system useful for modulating gene expression in host cell
PT for gene therapy and large-scale production of proteins and antibodies.
XX
PS Claim 4; Page 112; 123pp; English.
XX
CC The invention relates to a novel gene expression modulation system
CC comprising first and second gene expression cassettes that comprises
CC polynucleotides encoding first and second hybrid polypeptides. The gene
CC expression modulation system is useful for modulating the expression of a
CC gene in a host cell comprising the gene to be modulated, for applications
CC such as gene therapy, large-scale production of proteins and antibodies,
CC cell-based high throughput screening assays, functional genomics and
CC regulation of traits in transgenic organisms. This polynucleotide
CC sequence represents DNA relating to the gene expression cassettes of the
CC invention
XX
SQ Sequence 1288 BP; 318 A; 368 C; 346 G; 256 T; 0 U; 0 Other;

Query Match 100.0%; Score 1054; DB 6; Length 1288;
Best Local Similarity 100.0%; Pred. No. 1.6e-281;
Matches 1054; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGAGTGGCTAGTACCGGACTCAGTGGCCATGAAGCGGAAAGAGAGACACAG 60
Db 235 CCTGAGTGGCTAGTACCGGACTCAGTGGCCATGAAGCGGAAAGAGAGACACAG 294
QY 61 AAGGAGAGGACAACTGCGCTGTGACGACGACGCTGGACGACCATGCGCCCATTT 120
Db 295 AAGGAGAGGACAACTGCGCTGTGACGACGACGCTGGACGACCATGCGCCCATTT 354
QY 121 ATGCAGTGTGAACCTCCACTCTCTGAAGAGCAAGGATTCAAGAGTGGTCCCAAGTTT 180
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Db 355 ATGCAGTGTGAACCTCCACTCTCTGAAGAGCAAGGATTCAAGAGTGGTCCCAAGTTT 414
QY 181 CTCTCCGACAAAGCTGTGTGGAGCAAAACCGCGCAGAAAAAATCCCTCCAGTTTGACAGCCAAC 240
Db 415 CTCTCCGACAAAGCTGTGTGGAGCAAAACCGCGCAGAAAAAATCCCTCCAGTTTGACAGCCAAC 474
QY 241 CAGCAGTTCTTATTCGCCAGGCTCATCTGGTACACGAGACGGGTACGAGCAGCCTTCTGAT 300
Db 475 CAGCAGTTCTTATTCGCCAGGCTCATCTGGTACACGAGACGGGTACGAGCAGCCTTCTGAT 534
QY 301 GAAGATTTGAAGAGGATTACGACAGAGTGGCAGCAGCAGCAGCAGTGAACGAGAGTCT 360
Db 535 GAAGATTTGAAGAGGATTACGACAGAGTGGCAGCAGCAGCAGCAGTGAACGAGAGTCT 594
QY 361 GACACTCCCTTTCGCCAGATCAACAGAGATGACTATCTCTCAGCGTCCAACCTTATCGTGGAG 420
Db 595 GACACTCCCTTTCGCCAGATCAACAGAGATGACTATCTCTCAGCGTCCAACCTTATCGTGGAG 654
QY 421 TTCCGGAAGGATTGCCAGGTTTCGCCAGATCTCGCAGCCTGATCAAAATACGCTGCTT 480
Db 655 TTCCGGAAGGATTGCCAGGTTTCGCCAGATCTCGCAGCCTGATCAAAATACGCTGCTT 714
QY 481 AAGGCTTGTCTCAAGTGAAGGTAATGATGCTCCGAGTCCGCGACGATACGATCGGCTCA 540
Db 715 AAGGCTTGTCTCAAGTGAAGGTAATGATGCTCCGAGTCCGCGACGATACGATCGGCTCA 774
QY 541 GACAGTGTCTCTGTTCCGGAACAAACCAAGCGTACACTCGCGACAACTACCGCAAGGCTGGC 600
Db 775 GACAGTGTCTCTGTTCCGGAACAAACCAAGCGTACACTCGCGACAACTACCGCAAGGCTGGC 834
QY 601 ATGGCCTACGTCATCGAGGATCTACTGCACTTCTGCGGTGCACTGATCTCTATGGCGTTG 660
Db 835 ATGGCCTACGTCATCGAGGATCTACTGCACTTCTGCGGTGCACTGATCTCTATGGCGTTG 894
QY 661 GACACATCCATTACCGGCTGCTCAGCGCTGCTCATCTTTTCTGACCGCGCAGGTTG 720
Db 895 GACACATCCATTACCGGCTGCTCAGCGCTGCTCATCTTTTCTGACCGCGCAGGTTG 954
QY 721 GAGCAGCCGCAACTGGTGGAGAAATCCAGCGGTACTACTCTGAATACGCTCCGCACTAT 780
Db 955 GAGCAGCCGCAACTGGTGGAGAAATCCAGCGGTACTACTCTGAATACGCTCCGCACTAT 1014
QY 781 ATCTGAAACAGCTGAGCGGTCGGCGGTTCTGTCGTCTATATACGCGCAAGATCCTCTCA 840
Db 1015 ATCTGAAACAGCTGAGCGGTCGGCGGTTCTGTCGTCTATATACGCGCAAGATCCTCTCA 1074
QY 841 ATCTCTCTGAGCTAGCAGCTCGCGCTCGGCTGCAAACTCCAACTGTCATCTCCCTCAAG 900
Db 1075 ATCTCTCTGAGCTAGCAGCTCGCGCTCGGCTGCAAACTCCAACTGTCATCTCCCTCAAG 1134
QY 901 CTCAGAACACAAAGCTGCGGCTTTCTCTCGAGGAGATCTGGGATGTGGCGGACATGTCG 960
Db 1135 CTCAGAACACAAAGCTGCGGCTTTCTCTCGAGGAGATCTGGGATGTGGCGGACATGTCG 1194
QY 961 CACACCCAAACCGCGCTATCTCGAGTCCCCCAACGAATCTTAGCCCTCGCGCAGC 1020
Db 1195 CACACCCAAACCGCGCTATCTCGAGTCCCCCAACGAATCTTAGCCCTCGCGCAGC 1254
QY 1021 ATGCCGATCGCGGTCGGCCGGCTGCTCTGA 1054
Db 1255 ATGCCGATCGCGGTCGGCCGGCTGCTCTGA 1288

RESULT 12
ABK49451
ID ABK49451 standard; DNA; 1290 BP.
XX
AC AC
XX
DT 02-JUL-2002 (first entry)
XX
DE DNA encoding Choriostoneura fumiferana ecdysone receptor (CEBcr) #1.
XX
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KW Ecdysone; receptor; ECR; multiple inducible gene modulation system; proteomic; functional genomic; gene therapy; toxicology screening; large scale protein production; transactivation; biosensor; spruce budworm; ds.

OS Choristoneura fumiferana.

PN WO200229075-A2.

XX 11-APR-2002.

XX 28-SEP-2001; 2001WO-US030608.

XX 03-OCT-2000; 2000US-0237446P.

PR 27-SEP-2001; 2001US-00965697.

XX (ROHM) ROHM & HAAS CO.

XX Dhadialla TS, Cress DE, Carlson GR, Hormann RE, Palli SR; Kudla AJ, Herzig RP, Philip M;

XX MPI; 2002-352234/38.

DR A multiple inducible gene modulation system, for investigating multi-gene processes, comprises several individually operable gene modulation systems.

XX Example 1; Page 71; 79pp; English.

XX The invention describes a multiple inducible gene modulation system (I) comprising several individually operable gene modulation systems. It also useful in proteomics, functional genomics, gene therapy, cell-based high throughput assays, biosensor, toxicology screening and large scale protein production. Specifically, it allows investigation of complex multi-gene processes such as signal transduction cascades. It also enables regulation of multiple genes for gene therapy. In (I), because the binding and transactivation domains reside on two different molecules, the background activity in the absence of ligand is greatly reduced. It also provides improved sensitivity to non-steroidal ligands. Also since transactivation based on ecdysone receptor switches is often call-line dependent, it is easier to tailor switching systems to obtain maximum transactivation capability for each application. This sequence encodes the Choristoneura fumiferana ecdysone receptor (CfEcR) C (DNA binding), D (hinge), E (ligand binding) and F domains used in the creation of a gene expression cassette for use in the multiple inducible gene expression system

XX Sequence 1290 BP; 321 A; 364 C; 347 G; 258 T; 0 U; 0 Other;

Query Match 97.78; Score 1029.4; DB 6; Length 1290;

Best Local Similarity 99.74; Pred. No. 1e-274;

Matches 1052; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

QY 1 CCTGAGTGGCTAGTACCCGAGACTCAGTGGCCATGAAGCGGAAAGAGAAAGACACAG 60

DB 237 CCTGAGTGGCTAGTACCCGAGACTCAGTGGCCATGAAGCGGAAAGAGAAAGACACAG 296

QY 61 AAGGAGAAGGACAACTGCTGTGACGACGACGAGCGGTGGACGACCATGCGCCCATTT 120

DB 297 AAGGAGAAGGACAACTGCTGTGACGACGACGAGCGGTGGACGACCATGCGCCCATTT 356

QY 121 ATGCAAGTGTGAACCTCCACTCTGGAAGCAGCAAGGATTCAGAGTGGTCCCAAGTTT 180

DB 357 ATGCAAGTGTGAACCTCCACTCTGGAAGCAGCAAGGATTCAGAGTGGTCCCAAGTTT 416

QY 181 CTCTCCGACAAAGCTGTGGAGACAAACCGGACGAAAAACATCCCGCAGTTTGACAGCCAAC 240

DB 417 CTCTCCGACAAAGCTGTGGAGACAAACCGGACGAAAAACATCCCGCAGTTTGACAGCCAAC 476

QY 241 CAGCAGTTCCTTATCGCCAGGCTCATCTGGTACGAGCCGGTACGAGCCGCTTCTGAT 300

DB 477 CAGCAGTTCCTTATCGCCAGGCTCATCTGGTACGAGCCGGTACGAGCCGCTTCTGAT 536

QY 301 GAAGATTTTCAAGGATTTACGAGAGTGGCGAGCGGAGCGGAGATGAAACGAGAGTCT 360

DB 537 GAAGATTTTCAAGGATTTACGAGAGTGGCGAGCGGAGCGGAGATGAAACGAGAGTCT 596

QY 361 GACATCTCCCTTCCGCGAGATCACAGAGATGACTATCTCACGCTCCAACTTATTCGTGGAG 420

DB 597 GACATCTCCCTTCCGCGAGATCACAGAGATGACTATCTCACGCTCCAACTTATTCGTGGAG 656

QY 421 TTCGCGAAGGATTTCCGAGGTTTCGCAAGATCTCGAGCTCGAGCTGATCAAAATACGCTGCTT 480

DB 657 TTCGCGAAGGATTTCCGAGGTTTCGCAAGATCTCGAGCTCGAGCTGATCAAAATACGCTGCTT 716

QY 481 AAGGCTTTCCTCAAGTGAGTAAATGATCTCCGAGTGGCGGAGCGATACGATCGGCGCTCA 540

DB 717 AAGGCTTTCCTCAAGTGAGTAAATGATCTCCGAGTGGCGGAGCGATACGATCGGCGCTCA 776

QY 541 GACAGTGTTCCTTTCGCGAACAACCAAGCGTACACTCGCGGACAACTACCGCAAGGCTGGC 600

DB 777 GACAGTGTTCCTTTCGCGAACAACCAAGCGTACACTCGCGGACAACTACCGCAAGGCTGGC 836

QY 601 ATGGCTTTCCTCAAGTGAGTAAATGATCTCCGAGTGGCGGAGCGATACGATCGGCGCTTG 660

DB 837 ATGGCTTTCCTCAAGTGAGTAAATGATCTCCGAGTGGCGGAGCGATACGATCGGCGCTTG 896

QY 661 GACAACTCCATTTACGCGCTGCTCACGCGTGGCTCATCTTTTCTGACCGGCGGAGGTTG 720

DB 897 GACAACTCCATTTACGCGCTGCTCACGCGTGGCTCATCTTTTCTGACCGGCGGAGGTTG 956

QY 721 GACAGCCGCAACTGGTGGAGAAATCCAGCGGTACTACTGAAATACGCTCCGCACTCTAT 780

DB 957 GACAGCCGCAACTGGTGGAGAAATCCAGCGGTACTACTGAAATACGCTCCGCACTCTAT 1016

QY 781 ATCTGAAACAGCTGAGCGGTTGGCGGCTTTCGCTCATATACGCGAAGATCTCTCTCA 840

DB 1017 ATCTGAAACAGCTGAGCGGTTGGCGGCTTTCGCTCATATACGCGAAGATCTCTCTCA 1076

QY 841 ATCTCTCTGAGTACGCAAGCTGGGATGCAAACTCCAAACATGTCATCTCCCTCAAG 900

DB 1077 ATCTCTCTGAGTACGCAAGCTGGGATGCAAACTCCAAACATGTCATCTCCCTCAAG 1136

QY 901 CTCAAGACAGAAAGCTGGCGCTTTCCTCGAGGAGATCTGGGATGTGGC-GGACATGTC 959

DB 1137 CTCAAGACAGAAAGCTGGCGCTTTCCTCGAGGAGATCTGGGATGTGGCAGGACATGTC 1196

QY 960 GCACACCCAAACCGCCCTTATCTCGAGTCCCGCCACGAAATCTTAGCCCTTCGCGCACG 1019

DB 1197 GCACACCCAAACCGCCCTTAT-CTCGAGTCCCGCCACGAAATCTTAGCCCTTCGCGCACG 1255

QY 1020 CATCGCGGATGCGCGTCCGCGCGGCTGCTCTGA 1054

DB 1256 CATCGCGGATGCGCGTCCGCGCGGCTGCTCTGA 1290

RESULT 13

ACF36056

ID ACF36056 standard; DNA; 1290 BP.

XX ACF36056;

AC AC

XX AC

XX AC

DT 20-NOV-2003 (first entry)

XX

DE C. fumiferana ecdysone receptor (EcR) C, D, E and F domains DNA sequence.

XX

KW GAL4; DNA binding domain; DBD; gene expression; gene switch; EcR;

KW ecdysone receptor; ds.

XX Choristoneura fumiferana.

OS

PN WO2003060103-A2.

XX

PD 24-JUL-2003.

XX

PF 13-JAN-2003; 2003WO-US000915.

CC plants, flowers, fuels, therapeutic polypeptides, pathway intermediates,
CC for the modulation of pathways already existing in the host for the
CC synthesis of new products, cell based assays; functional genomics assays,
CC biotherapeutic protein production, proteomics assays. The present
CC sequence represents a C. fumiferana ecdysone receptor (EcR) related DNA
CC sequence
XX
SQ Sequence 1073 BP; 266 A; 319 C; 275 G; 213 T; 0 U; 0 Other;

Query Match 95.8%; Score 1010.2; DB 9; Length 1073;
Best Local Similarity 99.2%; Pred. No. 2e-269;
Matches 1047; Conservative 0; Mismatches 3; Indels 5; Gaps 3;

QY 1 CCTGAGTGGTAGTACCGGAGACTCAGTGGCCATGAAGCGGAAAGAGAAAGCAAG 60
DB |||||
QY 1 CCTGAGTGGTAGTACCGGAGACTCAGTGGCCATGAAGCGGAAAGAGAAAGCAAG 60
DB |||||
QY 61 AAGGAGAGGACAACTGCCCTGTCCAGCAGCAGCGGTGGACGACCATGCGCCCATTT 120
DB |||||
QY 61 AAGGAGAGGACAACTGCCCTGTCCAGCAGCAGCGGTGGACGACCATGCGCCCATTT 120
DB |||||
QY 121 ATGCAGTGTGAACCTCCACCTCTCTGAAGCAGCAAGGATTACAGAGTGGTCCCAAGGTTT 180
DB |||||
QY 121 ATGCAGTGTGAACCTCCACCTCTCTGAAGCAGCAAGGATTACAGAGTGGTCCCAAGGTTT 180
DB |||||
QY 181 CTCTCCGACAAAGCTGTGGAGACAAACCGGAGAGAAACATCCCCAGTTGACAGCCAAAC 240
DB |||||
QY 181 CTCTCCGACAAAGCTGTGGAGACAAACCGGAGAGAAACATCCCCAGTTGACAGCCAAAC 240
DB |||||
QY 241 CAGCAGTCTCTTATCGCCAGGCTCATCTGGTACGAGCGGTACGAGCGCTTCTGAT 300
DB |||||
QY 241 CAGCAGTCTCTTATCGCCAGGCTCATCTGGTACGAGCGGTACGAGCGCTTCTGAT 300
DB |||||
QY 301 GAAGATTGAAGAGGATTACGACAGCTGGCAGCAAGCGACGATGAAACGAAAGAGTCT 360
DB |||||
QY 301 GAAGATTGAAGAGGATTACGACAGCTGGCAGCAAGCGACGATGAAACGAAAGAGTCT 360
DB |||||
QY 361 GACATCTCTTCCGCCAGATCAGAGATGACTATCTCAGCGTCCAACTTATCGTGGAG 420
DB |||||
QY 361 GACATCTCTTCCGCCAGATCAGAGATGACTATCTCAGCGTCCAACTTATCGTGGAG 420
DB |||||
QY 421 TTCCGAGAGGATTCGAGGTTCCGAGATCTCGAGCTGATCAANTTACGCTGTT 480
DB |||||
QY 421 TTCCGAGAGGATTCGAGGTTCCGAGATCTCGAGCTGATCAANTTACGCTGTT 480
DB |||||
QY 481 AAGGCTTGTCAAGTGAAGTAAATGATCTCGAGTCCGCGACGATACGATGCGGCTCA 540
DB |||||
QY 481 AAGGCTTGTCAAGTGAAGTAAATGATCTCGAGTCCGCGACGATACGATGCGGCTCA 537
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QY 541 GACAGTGTCTGTTCGCGAAACAAAGCGTACACTCGCGACAACTACCGCAAGGCTGGC 600
DB |||||
QY 538 GACAGTGTCTGTTCGCGAAACAAAGCGTACACTCGCGACAACTACCGCAAGGCTGGC 597
DB |||||
QY 601 ATGCGCTACGTCATGAGGATCTACTGCACTTCTGCGGTCGATGATCTATGCGGTTG 660
DB |||||
QY 598 ATGCGCTACGTCATGAGGATCTACTGCACTTCTGCGGTCGATGATCTATGCGGTTG 657
DB |||||
QY 661 GACAAATCCATTAACGCGTGTCTCAGCGTGTGCTCATCTTTTCTGACCGGCGAGGTTG 720
DB |||||
QY 658 GACAAATCCATTAACGCGTGTCTCAGCGTGTGCTCATCTTTTCTGACCGGCGAGGTTG 717
DB |||||
QY 721 GAGCAGCGCAACTGTGTGGAAGAAATCCAGCGTACTACCTGAATACGCTCCGCTAT 780
DB |||||
QY 718 GAGCAGCGCAACTGTGTGGAAGAAATCCAGCGTACTACCTGAATACGCTCCGCTAT 777
DB |||||
QY 781 ATCTGAAACGAGCTGAGCGGTTCGGCGGTTCGTCGTCATATACGCGAAGATCTCTCA 840
DB |||||
QY 778 ATCTGAAACGAGCTGAGCGGTTCGGCGGTTCGTCGTCATATACGCGAAGATCTCTCA 837
DB |||||
QY 841 ATCTCTCTGAGCTACGCGCTCGGATGCAAAATCCAAACATGTCATCTCCCTCAAG 900
DB |||||
QY 838 ATCTCTCTGAGCTACGCGCTCGGATGCAAAATCCAAACATGTCATCTCCCTCAAG 897
DB |||||

QY 901 CTCAGAGACAGAAAGCTGCGGCTTTCTCGAGAGATCTGGGATGTGGC-GGACATGTC 959
DB |||||
QY 998 CTCAGAGACAGAAAGCTGCGGCTTTCTCGAGAGATCTGGGATGTGGCAGGACATGTC 957
DB |||||
QY 960 GCACACCCAAACCGCGCTATCTCGAGTCCCGCCACGAAATCTTAGCCCCCTGCGCGCACG 1019
DB |||||
QY 958 GCACACCCAAACCGCGCTAT-CTCGAGTCCCGCCACGAAATCTTAGCCCCCTGCGCGCACG 1016
DB |||||
QY 1020 CATCGCGGATGCGCGCTGCGCGCGCTGCTCTGA 1054
DB |||||
QY 1017 CATCGCGATGCGCGCTGCGCGCGCTGCTCTGA 1051
DB |||||

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Job time : 666 secs

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